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OM nucleic - nucleic search, using sw model

Run on: July 23, 2004, 05:01:30 ; Search time 9940 Seconds
(without alignments)
11376.456 Million cell updates/sec

Title: US-10-618-839-1
Perfect score: 2609
Sequence: 1 gctgatacacagttctgtc.....aaaaaaaaaaaaaaaaaaaaa 2609

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl.*

- 1: gb.ba.*
- 2: gb.htg.*
- 3: gb.in.*
- 4: gb.om.*
- 5: gb.ov.*
- 6: gb.pat.*
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- 41: em.htgo.other.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	2605	99.8	2609	6	AR399401	AR399401 Sequence
2	2605	99.8	2609	6	AX351497	AX351497 Sequence
3	2605	99.8	2609	6	AX676981	AX676981 Sequence
4	2605	99.8	2609	9	AF127763	AF127763 Homo sapi
5	2593	99.4	2608	6	AX367290	AX367290 Sequence
6	1820.2	69.8	1881	6	AX367207	AX367207 Sequence
7	1820.2	69.8	1881	9	AF166327	AF166327 Homo sapi
8	1516.2	58.1	1734	9	AF166328	AF166328 Homo sapi
9	1384.6	53.1	1548	9	HSA438989	HSA438989 Homo sapi
10	1307.8	50.1	1692	10	AF539799	AF539799 Mus muscu
11	1305	50.0	2577	6	AR399418	AR399418 Sequence
12	1305	50.0	2577	10	AF152963	AF152963 Rattus no
13	1182.8	45.3	2619	6	AR399430	AR399430 Sequence
14	1036.6	39.7	1353	10	AY174116	AY174116 Mus muscu
15	630.6	24.2	66424	9	HS146H21	Z83819 Human DNA s
16	588.4	22.6	1713	10	RNO295950	AJ295950 Rattus no
17	588.4	22.6	1714	10	MMU43384	U43384 Mus musculu
18	582.4	22.3	1857	4	AF323788	AF323788 Oryctolag
19	582	22.3	1713	10	AF298656	AF298656 Rattus no
20	582	22.3	4324	6	AX281787	AX281787 Sequence
21	582	22.3	4339	9	BC032720	BC032720 Homo sapi
22	579.4	22.2	4267	6	AR380834	AR380834 Sequence
23	579.4	22.2	4267	9	HSXCGD	X04011 Human mRNa
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25	573.6	22.0	1713	4	AF411135	AF411135 Bison bis
26	560	21.5	3527	5	BC054624	BC054624 Danio rer
27	559.4	21.4	1755	4	AB034192	AB034192 Tursiops
28	551.6	21.1	658	6	AX367208	AX367208 Sequence
29	551.6	21.1	658	6	AX676982	AX676982 Sequence
30	551.6	21.1	658	9	AF166326	AF166326 Homo sapi
31	532.6	20.4	2229	5	AB099894	AB099894 Takifugu
32	521.2	20.0	2044	6	AR399402	AR399402 Sequence
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34	521.2	20.0	2044	9	AF190122	AF190122 Homo sapi
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37	468.6	18.0	491	6	AX351480	AX351480 Sequence
38	460.6	17.7	573	6	AX341610	AX341610 Sequence
39	446.2	17.1	449	6	AX341527	AX341527 Sequence
40	426.4	16.3	1558	4	SSU02476	U02476 Sus scrofa
41	405.4	15.5	428	6	BD226778	BD226778 A novel m
42	395.6	15.2	1332	9	AF229177	AF229177 Homo sapi
43	385.8	14.8	517	4	OC271882	AF271882 Oryctolag
44	362.2	13.9	381	6	AX351286	AX351286 Sequence
45	331	12.7	331	6	AX247173	AX247173 Sequence

ALIGNMENTS

RESULT 1
AR399401
LOCUS AR399401 2609 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 1 from patent US 6620603.
ACCESSION AR399401
VERSION AR399401.1 GI:40141268
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 2609)
AUTHORS Lambeth,J.D., Griendling,K.K., Lassegue,B.P., Arnold,R.S. and Cheng,G.
TITLE Human mitogenic oxidase
JOURNAL Patent: US 6620603-A 1 16-SEP-2003;

FEATURES		Location/Qualifiers	
source	1..2609	99.8%; Score 2605; DB 6; Length 2609;	
		Best Local Similarity 100.0%; Pred. No. 0;	
		Matches 2609; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
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QY	61	CTCTGGGGTAGGTGTGTTTTTACATCTTAAAGGCTCACAGACCCTGCGCTGGACAA	120
Db	61	CTCTGGGGTAGGTGTGTTTTTACATCTTAAAGGCTCACAGACCCTGCGCTGGACAA	120
QY	121	ATGTTCCATCTCGAAGGACCTCTCCAGATCCGGATTCGTAATCTTCGCTGTCCTTA	180
Db	121	ATGTTCCATCTCGAAGGACCTCTCCAGATCCGGATTCGTAATCTTCGCTGTCCTTA	180
QY	181	GAAGGCTCCAAACCACTCTTGACAAATGGAAATCGGTGGTTAAACCACTGGTTTTTCAG	240
Db	181	GAAGGCTCCAAACCACTCTTGACAAATGGAAATCGGTGGTTAAACCACTGGTTTTTCAG	240
QY	241	TTTGTGTTCTGTTGTTGGTTAGGCTGAATGTTTTTCCCTGTTTGGATGTCCTTCCTGA	300
Db	241	TTTGTGTTCTGTTGTTGGTTAGGCTGAATGTTTTTCCCTGTTTGGATGTCCTTCCTGA	300
QY	301	AATATGAGAAGCGCGACAAATCTACTACAAAGAAATCTTGGTCAACATTCGGCCT	360
Db	301	AATATGAGAAGCGCGACAAATCTACTACAAAGAAATCTTGGTCAACATTCGGCCT	360
QY	361	GTCCCGAGCGTCTGCTCTCTGCTTGAATTTTAAACAGCAGCTGATCCTGCTTCTGTGT	420
Db	361	GTCCCGAGCGTCTGCTCTCTGCTTGAATTTTAAACAGCAGCTGATCCTGCTTCTGTGT	420
QY	421	GTGCGAATCTGCTGCTTCTGAGGCGCACCTGTCTCAATTTTGCAGCGCGACACTGAGAA	480
Db	421	GTGCGAATCTGCTGCTTCTGAGGCGCACCTGTCTCAATTTTGCAGCGCGACACTGAGAA	480
QY	481	AGCAATTTGATCACACCTCACCTCCACAGCTGGTGGCTATATGATCTGCCTACATA	540
Db	481	AGCAATTTGATCACACCTCACCTCCACAGCTGGTGGCTATATGATCTGCCTACATA	540
QY	541	CAGCTATTACATCATTTGCACACCTGTTTAACTTTTGAATTTTGAATTTTGAATTTTGA	600
Db	541	CAGCTATTACATCATTTGCACACCTGTTTAACTTTTGAATTTTGAATTTTGAATTTTGA	600
QY	601	CCACAGATGCTCCCTTGGCTCCTTCTCCAGCTTATCTCATGATGAGAAAGGGGG	660
Db	601	CCACAGATGCTCCCTTGGCTCCTTCTCCAGCTTATCTCATGATGAGAAAGGGGG	660
QY	661	GTTCTTGGCTTAAATCCATCCAGTCCCGAAACACGACAGTGGAGTATGTGACATTCACCA	720
Db	661	GTTCTTGGCTTAAATCCATCCAGTCCCGAAACACGACAGTGGAGTATGTGACATTCACCA	720
QY	721	GCCTTGGCTGCTCCTACTGGAGTATCATGACAAATAGCCTTTGATTTCTCATGGTAACTTCAG	780
Db	721	GCCTTGGCTGCTCCTACTGGAGTATCATGACAAATAGCCTTTGATTTCTCATGGTAACTTCAG	780
QY	781	CTACTGAGTTTCATCCGAGAGTATTTTGAAGTCTTCTGGTATCTCATGACCTTTTAA	840
Db	781	CTACTGAGTTTCATCCGAGAGTATTTTGAAGTCTTCTGGTATCTCATGACCTTTTAA	840
QY	841	TCCTTCTATATCTTGGCTTAGGATTCACGGCATTTGGTGAATTTGTCGGGGTCAACACAG	900
Db	841	TCCTTCTATATCTTGGCTTAGGATTCACGGCATTTGGTGAATTTGTCGGGGTCAACACAG	900
QY	901	AGGAGCATGAATGAGAGTCATCTCGCAAGTGTGCGAGATGCTTTTGGAGATGTGGGATG	960
Db	901	AGGAGCATGAATGAGAGTCATCTCGCAAGTGTGCGAGATGCTTTTGGAGATGTGGGATG	960

QY	961	ATCGTGAATCCACATGTGTAGGCGCCCTAAGTTTGAAGGGCATGCCCTCGTGTCTTTGGAAGT	1020
Db	961	ATCGTGAATCCACATGTGTAGGCGCCCTAAGTTTGAAGGGCATGCCCTCGTGTCTTTGGAAGT	1020
QY	1021	GGATCCTTGCACCGGTCAATCTTTATATCTGTGAAAGGATCCTCCGGTGTTTACCGCTCCC	1080
Db	1021	GGATCCTTGCACCGGTCAATCTTTATATCTGTGAAAGGATCCTCCGGTGTTTACCGCTCCC	1080
QY	1081	AGCAGAAGGTTGATTAACCAAGGTTGTATGCAACCCATCCAAAGTTTTCGAAATTCGAGA	1140
Db	1081	AGCAGAAGGTTGATTAACCAAGGTTGTATGCAACCCATCCAAAGTTTTCGAAATTCGAGA	1140
QY	1141	TGAAACAGCGTGGCTTTCAGCATGGAAGTGGGGCAGTATATCTTTGTAAATTCGCCCTCAA	1200
Db	1141	TGAAACAGCGTGGCTTTCAGCATGGAAGTGGGGCAGTATATCTTTGTAAATTCGCCCTCAA	1200
QY	1201	TCTCTCTCCTGGAATGGCATCCTTTTACTTTTACTTTTGAACCTCTGCTCCAGAGGAAGATTTCTTCT	1260
Db	1201	TCTCTCTCCTGGAATGGCATCCTTTTACTTTTACTTTTGAACCTCTGCTCCAGAGGAAGATTTCTTCT	1260
QY	1261	CCATTCATATCCGACAGCAGGGACCTGGACAGAAATCTCATTAAGGGCTTTCGAAACAC	1320
Db	1261	CCATTCATATCCGACAGCAGGGACCTGGACAGAAATCTCATTAAGGGCTTTCGAAACAC	1320
QY	1321	AATATTCCAAATTCCTCCAGGATTGAAGTGGATGTTCCCTTTGGGCACAGCAGTGCAGGATG	1380
Db	1321	AATATTCCAAATTCCTCCAGGATTGAAGTGGATGTTCCCTTTGGGCACAGCAGTGCAGGATG	1380
QY	1381	TTTTCCAGTATGAAGTGGCTGTGCTGTGTTGGAGCAGGAATTTGGGGTCAACCCCTTTGCTT	1440
Db	1381	TTTTCCAGTATGAAGTGGCTGTGCTGTGTTGGAGCAGGAATTTGGGGTCAACCCCTTTGCTT	1440
QY	1441	CTATCTTGAATTCATCTGTGTACAAATTCAGTCTGCAGACCAAACTCAAAACAAAA	1500
Db	1441	CTATCTTGAATTCATCTGTGTACAAATTCAGTCTGCAGACCAAACTCAAAACAAAA	1500
QY	1501	AGATCTATTCTTCTACTGATCTGCAGGGAGACAGGTGCCTTTCTCTGTTTCAACAACTGT	1560
Db	1501	AGATCTATTCTTCTACTGATCTGCAGGGAGACAGGTGCCTTTCTCTGTTTCAACAACTGT	1560
QY	1561	TGACTTCCCTGAAACAGAGATGAGGAATTAAGCAAAAGTGGGTTTCTTAACTACCGTC	1620
Db	1561	TGACTTCCCTGAAACAGAGATGAGGAATTAAGCAAAAGTGGGTTTCTTAACTACCGTC	1620
QY	1621	TCTTCTCACCGGATGGGACAGCAATATTTGTTGGTTCATGACGATTTAACTTGCACAGG	1680
Db	1621	TCTTCTCACCGGATGGGACAGCAATATTTGTTGGTTCATGACGATTTAACTTGCACAGG	1680
QY	1681	CCACTGCATCTGTGACAGGTCTGAAACAGAAAACCTCCTTTGGGAGACCAATGTGGGACA	1740
Db	1681	CCACTGCATCTGTGACAGGTCTGAAACAGAAAACCTCCTTTGGGAGACCAATGTGGGACA	1740
QY	1741	ATGAGTTTCTTAATAGTACTCCTCCACCCCAAGTCTGTAGTGGAGTTTCTTTATGTG	1800
Db	1741	ATGAGTTTCTTAATAGTACTCCTCCACCCCAAGTCTGTAGTGGAGTTTCTTTATGTG	1800
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Db	1801	GGCTCGGACTTTGGCAAGAGCCTCGCAATGTGTCAACCGATATTCAGTCTGGATC	1860
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Db	1861	CTAGAAAGGTTCAATCTCTATTCACAAAGAAAATTTTGTAGTTATAGGAATAAGGACGG	1920
QY	1921	TAACTGCAATTTTGCTCTCTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT	1980
Db	1921	TAACTGCAATTTTGCTCTCTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT	1980
QY	1981	TCGCAATTTTGTCTCTTTGTATTCCTTCAGTAATTTTCTTGTCT	

QY	961	ATCGTGAATCCCACTGTAGCGCCCTTAAGTTTGAAGGGCATCCCTCTGAGTCTTGAAGT	1020
Db	961	ATCGTGAATCCCACTGTAGCGCCCTTAAGTTTGAAGGGCATCCCTCTGAGTCTTGAAGT	1020
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Db	1081	AGCAGAAGGTTCGATTACCAAGTTTGTATGACCCATCCAAAGTTTGGAAATTCAGA	1140
QY	1141	TGAACAAGCGTGTCTTTCAGATGGAAGTGGGAGATATATCTTGTGTAAATTCGCCCTCA	1200
Db	1141	TGAACAAGCGTGTCTTTCAGATGGAAGTGGGAGATATATCTTGTGTAAATTCGCCCTCA	1200
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Db	1201	TCTCTCTCTGNAATGCGATCCTTTTACCTTTCACCTCTCTGCTCCAGAGGAGATTTCTTCT	1260
QY	1261	CCATTCCATATCCGAGCAGCGGACTGGAAGAAATCTCATAGGGCTTTCGAAACAAC	1320
Db	1261	CCATTCCATATCCGAGCAGCGGACTGGAAGAAATCTCATAGGGCTTTCGAAACAAC	1320
QY	1321	AATATTCACCAATTCACAGATTTGAAGTGGATGGTCCCTTTGGCAGCAGCAGTGGATG	1380
Db	1321	AATATTCACCAATTCACAGATTTGAAGTGGATGGTCCCTTTGGCAGCAGCAGTGGATG	1380
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Db	1981	TCTGCAATTTGTCTCTTTTGTATCTTCAATTAATTAATGAGTTATAGGAATTAAGGACGTA	2040

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Db	2461	ATCCCATATACCAACAGTGATGTTTACTGTCTACATTTTGATATGTTTATCCAG	2520
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GI:18616842			
SOURCE			
Homo sapiens (human)			
ORGANISM			
Homo sapiens			
REFERENCE			
AUTHORS			
Jiang, Y., Hepler, W. T., Clapper, J. D., Wang, A. and Secrist, H.			
TITLE			
Compositions and methods for the therapy and diagnosis of colon			
JOURNAL			
Patent: WO 0196390-A 244 20-DEC-2001;			
CORIXA CORPORATION (US)			
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Db	421	GTGCGAATCTGCTGTCCTTCTGAGGGGCACTGCTCAITTTTGCAGCGCACACTGAGAA	480
QY	481	AGCAATTGATCACACACTCACCTTCCACAGCTGTGGCTATATGATCTGCTTACATA	540
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Db	1321	AATATTCAACAAATCCAGGATTTGAAGTGGATGTTCCCTTTGGCAGCAGCAGGAGT	1380
QY	1381	TTTTCCAGTATGAAGTGGTGTGCTGGTGGAGCAGGAATTTGGGTCAACCCCTTTGCTT	1440
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LOCUS
DEFINITION Sequence 84 from Patent WO0206515.
ACCESSION AX367290
VERSION AX367290.1 GI:18855394
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1
AUTHORS Macina, R.A. and Sun, Y.
TITLE Method of diagnosing, monitoring, staging, imaging and treating colon cancer
JOURNAL Patent: WO 0206515-A 84 24-JAN-2002;
diadexus, Inc. (US)
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DEFINITION Homo sapiens NADPH oxidase homolog 1 long form (NOHL) mRNA,
alternatively spliced, complete cds.
ACCESSION AF166327
VERSION AF166327.1 GI:6672077
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 1881)
Mammalia; Eutheria; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS Banfi, B., Maturana, A., Jaconi, S., Arnaudeau, S., Laforge, T.,
Sinha, B., Ligeti, E., Demareux, N. and Krause, K.H.
TITLE A mammalian H+ channel generated through alternative splicing of
the NADPH oxidase homolog NOH-1
JOURNAL Science 287 (5450), 138-142 (2000)
MEDLINE 20082959
PUBMED 10615049
REFERENCE 2 (bases 1 to 1881)
Banfi, B., Maturana, A., Jaconi, S., Arnaudeau, S., Laforge, T.,
Sinha, B., Ligeti, E., Demareux, N. and Krause, K.H.
AUTHORS Direct Submission
TITLE Submitted (08-JUL-1999) Dept. of Geriatrics, Geneva University
JOURNAL Hospitals, 2, ch. du Petit-Bel-Air, Chene-Bourg CH-1225,
Switzerland

FEATURES
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RESULT 8
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 DEFINITION Homo sapiens NADPH oxidase homolog 1 long form variant (NOH1) mRNA,
 alternatively spliced, complete cds.
 ACCESSION AF166328
 VERSION AF166328.1 GI:6672079
 KEYWORDS Homo sapiens (human)
 SOURCE
 ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 1734)
 Banfi, B., Maturana, A., Jaconi, S., Arnaudeau, S., Laforge, T.,
 Sinha, B., Ligeti, B., Demaurex, N. and Krause, K.H.
 A mammalian H⁺ channel generated through alternative splicing of
 the NADPH oxidase homolog NOH-1
 Science 287 (5450), 138-142 (2000)
 20082959
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 2 (bases 1 to 1734)
 Banfi, B., Maturana, A., Jaconi, S., Arnaudeau, S., Laforge, T.,
 Sinha, B., Ligeti, B., Demaurex, N. and Krause, K.H.
 Direct Submission
 Submitted (08-JUL-1999) Dept. of Geriatrics, Geneva University
 Hospitals, 2, ch. du Petit-Bel-Air, Chene-Bourg CH-1225,
 Switzerland

FEATURES

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ORIGIN

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RESULT 9
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LOCUS      Homo sapiens mRNA for noxi NAD(P)H-oxidase subunit (NOX1 gene).
DEFINITION      AJ438989
ACCESSION      AJ438989.1 GI:19572339
VERSION      NOX1 gene; noxi NAD(P)H-oxidase.
KEYWORDS      Homo sapiens (human)
SOURCE      Homo sapiens
ORGANISM      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
      Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE      1
AUTHORS      Haenze, J.
TITLE      NOX-1 is expressed in pulmonary cells
JOURNAL      Unpublished
REFERENCE      2 (bases 1 to 1548)
AUTHORS      Haenze, J.
TITLE      Direct Submission
JOURNAL      Submitted (13-MAR-2002) Haenze J., Internal Medicine II /
      Biochemistry, University of Giessen, Friedrichstr. 24, 35392,
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DEFINITION	Mus musculus NADPH oxidase 1 alpha mRNA, complete cds.	
ACCESSION	AF539799	
VERSION	AF539799.1 GI:25573159	
KEYWORDS		
SOURCE	Mus musculus (house mouse)	
ORGANISM	Mus musculus	
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
AUTHORS	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.	
TITLE	1 (Bases 1 to 1692)	
	Banfi,B., Clark,R.A., Steger,K. and Krause,K.-H.	
	Two Novel Proteins Activate Superoxide Generation by the NADPH	
JOURNAL	Oxidase NOX1	
PUBMED	J. Biol. Chem. 278 (6), 3510-3513 (2003)	
REFERENCE	12473664	
	2 (bases 1 to 1692)	

AUTHORS Banfi, B. and Krause, K.-H.
 TITLE Direct Submission
 JOURNAL Submitted (21-AUG-2002) Dept. of Geriatrics, University Hospitals of Geneva, Chemin du Petit-Bel-Air 2, Geneva CH-1225, Switzerland

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DEFINITION	Sequence 22 from patent US 6620603.						
ACCESSION	AR399418						
VERSION	AR399418.1	GI:40141300					
KEYWORDS	Unknown.						
SOURCE	Unknown.						
ORGANISM	Unclassified.						
REFERENCE	1 (bases 1 to 2577)						
AUTHORS	Lambeth, J.D., Griendling, K.K., Lassegue, B.P., Arnold, R.S. and Cheng, G.						
TITLE	Human mitogenic oxidase						
JOURNAL	Patent: US 6620603-A 22 16-SEP-2003;						
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Best Local Similarity	83.4%;	Pred. No. 1.3e-289;					
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QY	372	CTGCTCTCTGCTTGAATTTTACAGACGCTGATCTCTGCTTCTGTTGTGCGAATCTG	431	QY	1452	TCCATCTGGTCAAAATTCAGTGTGACAGCAACAACCTCAAAACAACCAAAAGATCTATTC	1511
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QY	552	ATCATGACACCTGTTTAACTTTGATCTGCTATAGAGAGCGGACAGCCACAGATGC	611	QY	1632	GGATGGGACAGCAATTTGTTGATCAGCAATTAACCTTTTGAACAGCCCACTGACATC	1691
Db	473	ATCATGACACCTGTTTAACTTTGATCTGCTATAGAGAGCGGACAGCCATGATGGA	532	Db	1550	GGCTGGATAGCAACATTTGCTGGTTCATGCAGCATTTAAACTTTGACAGAGCCAC	1609
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QY	672	AATCCATCCAGTCCGAAACACGAGTGGAGTATGTGACATTCACAGCGCTTCTGCTGT	731	QY	1752	ACAATAGTACTCTCCACCCCAAGTCTGTAGTGGGAGTTTCTTATGTGGCCCTCGGACT	1811
Db	590	AATCCATCCAGTCTCCAAACGTGACAGTATGATGATGAGCAATTTACAGTATTCCTGCG	649	Db	1670	AGAATAGTACTGCCCCACCCCAAGTCTGTGTGGGGTTTCTTATGCGGCCCTCCGACT	1729
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LOCUS		2577 bp mRNA linear ROD 06-OCT-1999		
DEFINITION		Rattus norvegicus NADH/NADPH mitogenic oxidase subunit p65-mox		
ACCESSION		AF152963		
VERSION		1		
KEYWORDS		complete cds.		
SOURCE		AF152963.1 GI:5081797		
ORGANISM		Rattus norvegicus (Norway rat)		
REFERENCE		1 (bases 1 to 2577)		
AUTHORS		Suh, Y.A., Arnold, R.S., Lassegue, B., Shi, J., Xu, X., Sorescu, D., Chung, A.B., Griending, K.K. and Lambeth, J.D.		
TITLE		Cell transformation by the superoxide-generating oxidase Mox1		
JOURNAL		Nature 401 (6748), 79-82 (1999)		
MEDLINE		99413719		
PUBMED		10485709		
REFERENCE		2 (bases 1 to 2577)		
AUTHORS		Lassegue, B.		
TITLE		Direct Submission		
JOURNAL		Submitted (19-MAY-1999) Cardiology, Emory University, 1639 Pierce		
DRIVE		Drive, 319 WMB, Atlanta, GA 30322, USA		
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ORIGIN				
Query Match		50.08; Score 1305; DB 10; Length 2577;		
Best Local Similarity		83.48; Pred. No. 1.3e-289;		
Matches 1495; Conservative		0; Mismatches 295; Indels 3; Gaps 1;		
QY	132	CTGAAGGACCTCCAGAAATCCGATGCTGGAATCTTCCCTGTGTCCTAGAGGCTCCA	191	
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QY	192	AACACCTCTTGACAAATGGGAACTGGTGGTTAAACCACTGGTTTCAGTTTGTGTTCTG	251	
Db	113	GACCTCCATTTGACAAATGGGAACTGGTGGTTAAACCACTGGTCTCAGTTTGTGTTCTG	172	
QY	252	GTGTTTGGTTAGGGCTGAATGTTTCTCTGTTGATGATCGCTTCCTGAAATATGAGAAG	311	
Db	173	GTTCCTTGGTTGGGGCTGAACATTTTCTGTTGTGTGACGTCCTCTCTGAAATATGAGAAG	232	
QY	312	CGCGACAAATACTACTACAGAGAAATTCCTGGGTCAACATTTGGCTGTGCCCGAGCG	371	
Db	233	TCTGACAAAGTACTATTACAGAGAGAAATTCCTGGAACCTGCTTGGCTTGGCCAGAGCA	292	
QY	372	TCTGCTCTCTGCTTGAATTTTAAACAGACGCTGATCTCTGCTTCTGTTGTGTCGAATCTG	431	
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RESULT 13
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LOCUS AR399430 2619 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 41 from patent US 6620603.
ACCESSION AR399430
VERSION AR399430.1 GI:40141322
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 2619)
AUTHORS Lambeth, J.D., Griendling, K.K., Lassegue, B.P., /; Cold, R.S. and
Cheng, G.
TITLE Human mitogenic oxidase
JOURNAL Patent: US 6620603-A 41 16-SEP-2003;
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Best Local Similarity 84.8%; Pred. No. 1.8e-261;
Matches 1338; Conservative 0; Mismatches 237; Indels 3; Gaps 1;

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RESULT 14
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 DEFINITION Mus musculus NOX1 (Nox1) mRNA, partial cds.
 ACCESSION AY174116
 VERSION AY174116.1 GI:27762622
 KEYWORDS
 SOURCE Mus musculus (house mouse)
 ORGANISM
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 REFERENCE
 AUTHORS Matsumoto, Y. and Blanchard, T. G.
 TITLE Nox1 expression in the gastric mucosa of Helicobacter-infected gp1phox-/- mice
 JOURNAL Unpublished
 AUTHORS Matsumoto, Y. and Blanchard, T. G.
 TITLE Direct Submission
 JOURNAL Submitted (06-NOV-2002) Pediatrics, Case Western Reserve University, 2101 Adelbert Road, Cleveland, OH 44106, USA
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ORIGIN
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 Best Local Similarity 85.8%; Pred. No. 8.3e-228;
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 Db 122 AAGAAGCCAACA 3GCCATGGATGATCTCTCGCTCTGTGTTCTCTCCAGCCTATCTCATCC 181
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 QY 1067 GTTTTACCCTCCACAGAGAAGTTGTGATTACCAAGTTTGTATCACCCATCCCAAGT 1126
 Db 599 CTTTATCCCTCCACAGAGAAGTGTGATTACCAAGTTGTATCACCCATCCATATATGT 658
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 Db 719 AAATTTGCCCTCAATCTCTCTCTGAGTGGCATCTCTTCACTCTGACTTCTGCTCCAGA 778
 QY 1247 GGAAGATTTCTTCTCCATTCATATCCGAGCAGCGGGACTGGACAGAAATCTCATAAG 1306
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 QY 1367 AGCAGTGAAGATGTTTTCCAGTATGAAGTGTGCTGTCTGTTGGAGAGGATTTGGGCT 1426
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 Db 959 CACTCCCTTTGCTTCCATCTTGAATCTATCTGTTACAAATTTCCAGCGTGGCGACAA 1018
 QY 1487 CCTCAAAACAAAAGATCTATTTCTACTGGATCTGCGAGGAGACAGGTGCCTTTTCCCTG 1546
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QY 1727 ACCAATGGGGACAATAGATTTTCTACAACTAGTCTCCACCCCAAGTCTGTAGTGGG 1786

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QY 1787 AGTTTCTTATGTCCTCGACTTGGCAAGA 1821

Db 1319 GGTTCCTTATGTCCTCGACTTGGCAAAA 1353

RESULT 15

LOCUS HSI146H21/c

DEFINITION Human DNA sequence from clone RPI-146H21 on chromosome Xq22

Contains cleavage stimulation factor, 64 KD subunit, gene similar to CYTOCHROME B-245 HEAVY CHAIN. pseudogene similar to hmrNP A1 protein and ESTs, complete sequence.

ACCESSION Z83819

VERSION Z83819.1 GI:3980337

KEYWORDS HTG; CSTF2; CYTOCHROME B.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 66424)

LAOYD, D.

Direct Submission

Submitted (05-JUN-2003) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquerry@sanger.ac.uk

humquerry@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk

On Dec 8, 1998 this sequence version replaced gi:3559852.

----- Genome Center

Center: Wellcome Trust Sanger Institute

Center code: SC

Web site: <http://www.sanger.ac.uk>

Contact: humquerry@sanger.ac.uk

During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest, except on the rare occasion of the clone being a YAC.

The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:

Em: EMBL; Sw: SWISSPROT; Tr: TrEMBL; Wp: WORMPEP; Information on the WORMPEP database can be found at http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome X, constructed by the Sanger Centre Chromosome X Mapping Group. Further information can be found at <http://www.sanger.ac.uk/HGP/ChrX>

RPI-146H21 is from the library RPCI-1 constructed by the group of Pieter de Jong. For further details see <http://www.chori.org/bacpac/home.htm>

VECTOR: pCVPAC2

IMPORTANT: This sequence is not the entire insert of clone RPI-146H21. It may be shorter because we sequence overlapping sections only once, except for a short overlap.

The true left end of clone RPI-146H21 is at 1 in this sequence. The

true left end of clone LLOXNC01-131B10 is at 66325 in this sequence. The true right end of clone RP3-347M6 is at 25559 in this sequence.

FEATURES

source Location/Qualifiers

1..66424

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/db_xref="RZPD:RCPID704H21146"

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/chromosome="X"

/map="q22"

/clone="RPI-146H21"

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/note="match: STS: Em:M85085"

677..4270

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/evidence=not experimental

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/note="35 copies 2 mer tt 67% conserved"

complement(1589..1704)

/note="match: STS: Em:AA422081"

2304..2604

/note="AluDb repeat: matches 1..300 of consensus"

3294..3369

/note="L1MD3 repeat: matches 7662..7739 of consensus"

3640..3867

/note="MER20 repeat: matches 2..218 of consensus"

4068..4270

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7655..7759

/note="MIR repeat: matches 6..117 of consensus"

7760..8069

/note="AluSx repeat: matches 2..312 of consensus"

8070..8215

/note="MIR repeat: matches 117..240 of consensus"

8393..8949

/note="L1MB7 repeat: matches 5606..6165 of consensus"

8950..9131

/note="AluSg repeat: matches 141..302 of consensus"

9132..9423

/note="AluY repeat: matches 1..293 of consensus"

9424..9558

/note="AluSg repeat: matches 1..141 of consensus"

9559..9708

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9960..9991

/note="16 copies 2 mer tc 93% conserved"

10034..10244

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10245..10543

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10544..10598

/note="MIR repeat: matches 13..70 of consensus"

10821..11123

/note="AluSg repeat: matches 1..302 of consensus"

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/pseudo
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repeat_region 25014..25259
/note="MIR repeat: matches 6..262 of consensus"
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repeat_region 26364..26422
/note="L2 repeat: matches 2687..2743 of consensus"
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Query Match

24.2%; Score 630.6; DB 9; Length 66424;

Best Local Similarity 91.3%; Pred. No. 2.7e-134;
 Matches 735; Conservative 0; Mismatches 8; Indels 62; Gaps 4;

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Qy	1832	ATGCTGTCACCGATATTCAGTCTGGATCTAGAAAGGTTCAATTCATCTCAACAAGA	1891
Db	7359	ATGCTGTCACCGATATTCAGTCTGGATCTAGAAAGGTTCAATTCATCTCAACAAGA	7300
Qy	1892	AAATTTTGTAGTATAGGAATAAGCAGGTAATCTGCATTTTGTCTTGTATCTTCAG	1951
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Qy	1952	TAATGTAGTTATAGGAATAAGCAGGTAATCTGCATTTTGTCTTGTATCTTCAGTAA	2011
Db	7293	---TTGAGTTATAGGAATAAGCAGGTAATCTGCATTTTGTCTTGTATCTTCAGTAA	7237
Qy	2012	TTTACTTTGGTCTCMTGAGGTTTGANCACTCAGTCTTAGGATAAGATGTGCTCTCAAGCC	2071
Db	7236	TTTACTTTGGTCTCMTGAGGTTTGANCACTCAGTCTTAGGATAAGATGTGCTCTCAAGCC	7177
Qy	2072	TTGACTCCCTGGTATCTTTTGTATTGATTGCAATCAACTTCGTTACTTTGAGCTTCAGCAAC	2131
Db	7176	TTGACTCCCTGGTATCTTTTGTATTGATTGCAATCAACTTCGTTACTTTGAGCTTCAGCAAC	7117
Qy	2132	TTAAGAACTTCTGAAAGTTCTTAAAGTTCTTAAAGCTTCTTAAAGCCCATGGATCTTCTCA	2191
Db	7116	TTAAGAACTTCTGAAAGTTCTTAAAGTTCTTAAAGCTTCTTAAAGCCCATGGATCTTCTCA	7057
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Qy	2252	TTTGGTGGTTCAANAATTATACAACTAATCCAGGTGATTTTATCAATTCAGTGTACCA	2311
Db	6996	TTTGGTGGTTCAAGTTATACAACTAATCCAGGTGATTTTATCAATTCAGTGTACCA	6937
Qy	2312	TCCTCTGAGTTTGGTTTGAATCTTTTGTCCCTCCACCCACACAGAAATTTT-TAAGT	2370
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Qy	2431	TAAATAATAACAATAATTTACCGAGAACCCCATCCCATATAACACCAAGTGTACATGT	2490
Db	6816	TAAATAATAACAATAATTTACCGAGAACCCCATCCCATATAACACCAAGTGTACATGT	6757
Qy	2491	TTACTGTCACTTTTGATATGGT-TTATCCAGTGTGAACAGCAATTTA---TTATTTTTC	2546
Db	6756	TTACTGTCACTTTTGATATGGT-TTATCCAGTGTGAACAGCAATTTTATTCTTATTTTTC	6697
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Search completed: July 23, 2004, 11:33:18
 Job time : 9959 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: July 23, 2004, 05:01:18 ; Search time 1001 Seconds
(without alignments)
11072.476 Million cell updates/sec

Title: US-10-618-839-1
Perfect score: 2609
Sequence: 1 gctgatagcacagtctctgtc.....aaaaaaaaaaaaaaaaaaaaa 2609

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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1: geneseqn1980s.*
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4: geneseqn2001as.*
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10: geneseqn2004as.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	2605	99.8	2609	3	AAD00692 Human mit
2	2605	99.8	2609	6	ABQ57805 Human col
3	2605	99.8	2609	7	ADA83892 Human NOX
4	2593	99.4	2608	6	ABK37993 Human col
5	1820.2	69.8	1881	6	ABK37991 Human col
6	1305	50.0	2577	3	AAD00694 Rat mitog
7	1182.8	45.3	2619	3	AAD00695 Rat mitog
8	630.6	24.2	7517	4	AAK89061 Human dig
9	587.6	22.5	1192	4	AAK87743 Human dig
10	582	22.3	4266	7	ACC00438 Human gp9
11	582	22.3	4324	6	AAS94941 Human DNA
12	579.4	22.2	4267	6	ABK84501 Human col
13	551.6	21.1	658	6	ABK37992 Human col
14	551.6	21.1	658	6	ADA83893 Human NOX
15	521.2	20.0	2044	3	AAD00693 Human mit
16	521.2	20.0	2044	3	AAL50289 Human col
17	501.2	19.2	560	6	ABQ58274 Human col
18	479.2	18.4	503	7	AAD55537 Human col
19	478.8	18.4	558	6	ABL36930 Human col
20	468.6	18.0	491	6	ABK27790 Human col
21	468.6	18.0	562	6	ABQ58190 Human col
22	460.6	17.7	573	6	ABL38268 Human col
23	446.2	17.1	449	6	ABL38185 Human col

24	423.6	16.2	579	6	ABQ57805 Human col
25	418	16.0	586	6	ABQ58832 Human col
26	414.2	15.9	3435	5	AAS69253 DNA encod
27	409.4	15.7	3435	5	AAS68641 DNA encod
28	405.4	15.5	428	3	AZ45660 DNA sequ
29	386.4	14.8	493	4	AAH35144 Human col
30	383	14.7	519	6	ABQ57452 Human col
31	371.6	14.2	509	6	ABQ57779 Human col
32	362.2	13.9	381	6	ABK27596 Human col
33	333.8	12.8	447	6	ABQ59120 Human col
34	331	12.7	331	4	AAS39045 Novel hum
35	326.8	12.5	339	4	AAS39162 Novel hum
36	322.4	12.3	464	6	ABQ59160 Human col
37	319.8	12.3	399	5	AAF64565 Novel hum
38	303	11.6	894	6	ABK27798 Human col
39	298.8	11.5	316	6	ABK44925 CDNA enco
40	296.2	11.4	609	6	ABQ58062 Human col
41	249.2	9.6	323	4	AAS37989 Novel hum
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44	84.6	3.2	2766	6	ABZ12979 Arabidops
45	84.6	3.2	2766	7	ADA68503 Arabidops

ALIGNMENTS

RESULT 1
AAD00692
ID AAD00692 standard; cDNA; 2609 BP.
XX
AC AAD00692;
XX
DT 08-SEP-2000 (first entry)
XX
DE Human mitogenic regulator mox1 cDNA.
XX
KW Human; mitogenic regulator; mox1; mitogenic oxidase; p65mox; superoxide;
KW reactive oxygen intermediate; ROI; cell division; cytosolic;
KW antiproliferative; cardiant; antiarteriosclerotic; vasotrophic;
KW angiogenic; hypotensive; drug development; treatment; cancer;
KW abnormal growth; peoriasis; prostatic hypertrophy; proliferation;
KW blood vessel; lymphatic vessel; benign prostatic hypertrophy;
KW cardiovascular disease; arteriovenous malformation; eye disorder;
KW hypertension; atherosclerosis; restenosis; angioplasty; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
CDS 207..1901
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WO200028031-A2.
XX
18-MAY-2000.
XX
10-NOV-1999; 99WO-US026592.
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10-NOV-1998; 98US-0107911P.
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27-AUG-1999; 99US-0151242P.
(UYEM-) UNIV EMORY.
XX
Lambeth JD, Lassegue BP, Griending KK, Arnold RS, Guangjie C;
WPI; 2000-376545/32.
XX
P-PSDB; AAV71119.
XX
Protein capable of stimulating superoxide production, useful for treating
conditions associated with abnormal growth, including cancer.

XX
PS Claim 4; Page 79-83; 141pp; English.
XX
CC The present sequence is a cDNA encoding human mitogenic oxidase mox1,
CC also referred as p6smox, which is capable of stimulating production of
CC superoxide, a reactive oxygen intermediate (ROI) that affects cell
CC division. The mox1 protein functions as a mitogenic regulator and shows
CC homology to gp91phox protein. It is highly expressed in colon. The
CC present sequence is useful in developing drugs and therapies for
CC treatment of conditions associated with abnormal growth, including
CC cancer, psoriasis, prostatic hypertrophy, benign prostatic hypertrophy,
CC cardiovascular disease, proliferation of vessels, e.g. blood vessels and
CC lymphatic vessels, arteriovenous malformation, vascular problems
CC associated with eye, atherosclerosis, hypertension, and restenosis
CC following angioplasty
XX
SQ Sequence 2609 BP; 703 A; 574 C; 549 G; 779 T; 0 U; 4 Other;
Query Match 99.8%; Score 2605; DB 3; Length 2609;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2609; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 1 GCTGATAGCACAGTCTCTGTCAGAGAGGAAGGGGGAATAAACTATTTCATTCACAGAA 60
Qy 61 CTCTTGGGTAGGTGTGTGTTTTTTCACATCTTAAAGGCTACAGACCCTGGCTGGACAA 120
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Db 181 GAAGGGCTCCAAACACCTCTTGACAATGGGAAACTGGGTGTTAAACCACTGGTTTCAG 240
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Qy 601 CCAGATGGTCCCTTCCCTCCATTCCTCAGGCTATCTCATGATCAGAAAAAGGGGG 660
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Db 661 GTTCTTGGCTAAATCCCATCCAGTCCCGAAACACACAGAGTGGAGTATGTCATTCACCA 720
Qy 721 GGGTTGCTGGTCTCACTGGAGTGATCATGACATAGCCTTGAATTCATGTTAACTTCAG 780
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Qy 781 CTACTGAGTCTATCCCGAGGAGTATTATTTGAGTCTTTCTGGTATACTCACACCTTTTAA 840
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Db 901 AGGAGAGCATGATGATGAGAGTATCCTCGAAGTGTGAGAGTCTTTTGAAGTGTGGAGT 960
Qy 961 ATCGTGTACTCCCACTGTAGGCGCCCTAAGTTTGAAGGGCATCCCCCTGAGTCTTGGAGT 1020
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Db 1141 TGAACAAAGCGTGGCTTCAGCATGGAAGTGGGCGAGTATCTTTGTTAAATTCGCCCTCAA 1200
Qy 1201 TCTCTCTCTGCAATGGCATCCTTTTACTTTTACCTCTGTCTCCAGAGGAAGATTTCTTCT 1260
Db 1201 TCTCTCTCTGCAATGGCATCCTTTTACTTTTACCTCTGTCTCCAGAGGAAGATTTCTTCT 1260
Qy 1261 CCATTCATATCCGAGCAGCGGACCTGGACAGAAATCTCATAGGGCTTTTCGAACAAAC 1320
Db 1261 CCATTCATATCCGAGCAGCGGACCTGGACAGAAATCTCATAGGGCTTTTCGAACAAAC 1320
Qy 1321 AATATTCACCAATTTCCAGAGGATTCAGTGAATGCTTCCCTTTGGCACAGCCAGTGGAGT 1380
Db 1321 AATATTCACCAATTTCCAGAGGATTCAGTGAATGCTTCCCTTTGGCACAGCCAGTGGAGT 1380
Qy 1381 TTTTCCAGTATCAAGTGGCTGTGTTGGAGCAGGAATTTGGGTTCACCCCTTTGCTT 1440
Db 1381 TTTTCCAGTATCAAGTGGCTGTGTTGGAGCAGGAATTTGGGTTCACCCCTTTGCTT 1440
Qy 1441 CTATCTTGAATTCATCTGGTACAAATTCAGTGTGAGACCAACCTCAAAACAAA 1500
Db 1441 CTATCTTGAATTCATCTGGTACAAATTCAGTGTGAGACCAACCTCAAAACAAA 1500
Qy 1501 AGATCTATTTCTTCTGGAATCTGCAGGAGACAGAGTGCCTTTTCTGGTTCAACACCTGT 1560
Db 1501 AGATCTATTTCTTCTGGAATCTGCAGGAGACAGAGTGCCTTTTCTGGTTCAACACCTGT 1560
Qy 1561 TGACTTCCCTCGAAACAGGAGATGGAGAAATTTAGGCAAGTGGGTTTTCTAAACTACCGTC 1620
Db 1561 TGACTTCCCTCGAAACAGGAGATGGAGAAATTTAGGCAAGTGGGTTTTCTAAACTACCGTC 1620
Qy 1621 TCTTCCCTCAGCGATGGGACAGCAATATTGTTGGTATGACGATTAACCTTTGACAAGG 1680
Db 1621 TCTTCCCTCAGCGATGGGACAGCAATATTGTTGGTATGACGATTAACCTTTGACAAGG 1680
Qy 1681 CCACTGACATCTGACAGGTCTGAAACAGAAAAAACCCTCTTTGGGAGACCAATTTGGGACA 1740
Db 1681 CCACTGACATCTGACAGGTCTGAAACAGAAAAAACCCTCTTTGGGAGACCAATTTGGGACA 1740
Qy 1741 ATGAGTTTTCTCAATAGTACTCTCCACCCCAAGTCTGTAGTGGAGTTTTCTTATGTG 1800
Db 1741 ATGAGTTTTCTCAATAGTACTCTCCACCCCAAGTCTGTAGTGGAGTTTTCTTATGTG 1800
Qy 1801 GCCCTCGACTTTGGCAAGAGCCCTCGCAATGCTGTCAACGATATTCAGTCTGGATC 1860
Db 1801 GCCCTCGACTTTGGCAAGAGCCCTCGCAATGCTGTCAACGATATTCAGTCTGGATC 1860

Db 361 GTGCCCAGCGTCTGCTCTCTGCTTGAAATTTTAAACAGCAGCGTGATCCTGCTTCTGCTGT 420
 Qy 421 GTCCCAATCTGCTCTCTCTCTGAGGGGCACCTCTCATTTTTCAGCGGCACACTGAGAA 480
 Db 421 GTCCCAATCTGCTCTCTCTCTGAGGGGCACCTCTCATTTTTCAGCGGCACACTGAGAA 480
 Qy 481 AGCAATTTGGATCAAACTCACTTCCACAAAGCTGGTGGCCTATATGATCTGCCCTACATA 540
 Db 481 AGCAATTTGGATCAAACTCACTTCCACAAAGCTGGTGGCCTATATGATCTGCCCTACATA 540
 Qy 541 CAGCTATTACATCATTTGCAACACTGTTTAACTTTTGAATCTATAGCAGAAAGCCGACAGG 600
 Db 541 CAGCTATTACATCATTTGCAACACTGTTTAACTTTTGAATCTATAGCAGAAAGCCGACAGG 600
 Qy 601 CCACAGATGGCTCCCTTGGCTCCATTTCTCTCCAGCCTATCTCATGATGAGAAAAAGGGGG 660
 Db 601 CCACAGATGGCTCCCTTGGCTCCATTTCTCTCCAGCCTATCTCATGATGAGAAAAAGGGGG 660
 Qy 661 GTTCTTGGCTAAATCCCATCCAGTCCCGAAACACAGCAGTGGAGTATGACATTTCAACA 720
 Db 661 GTTCTTGGCTAAATCCCATCCAGTCCCGAAACACAGCAGTGGAGTATGACATTTCAACA 720
 Qy 721 GCGTTGCTGCTCTCACTGGAGTGATCATGACAAATAGCCTTGATTTCTCATGCTTAACCTT 780
 Db 721 GCGTTGCTGCTCTCACTGGAGTGATCATGACAAATAGCCTTGATTTCTCATGCTTAACCTT 780
 Qy 781 CTACTGAGTTTCATCCGGAGGAGTTATTTTGAAGTCTTCTGATATCTCAACCTTTTATA 840
 Db 781 CTACTGAGTTTCATCCGGAGGAGTTATTTTGAAGTCTTCTGATATCTCAACCTTTTATA 840
 Qy 841 TCTTCTATATCTTGGCTTAGGATTCACGGATTTGGTGGAAATGTCGGGGTCAACAG 900
 Db 841 TCTTCTATATCTTGGCTTAGGATTCACGGATTTGGTGGAAATGTCGGGGTCAACAG 900
 Qy 901 AGGAGCATGAATCAGAGTCACTCTCGCAAGTGTGCAGAGTCTTTTTCAGATGTGGGATG 960
 Db 901 AGGAGCATGAATCAGAGTCACTCTCGCAAGTGTGCAGAGTCTTTTTCAGATGTGGGATG 960
 Qy 961 ATCGTACTCCCATCTGTAGGCGCCCTAAATTTGAAGGAGTCCCTCGAGTCTTGGAAAGT 1020
 Db 961 ATCGTACTCCCATCTGTAGGCGCCCTAAATTTGAAGGAGTCCCTCGAGTCTTGGAAAGT 1020
 Qy 1021 GGATCTTTCACCGCTCATCTTTATCTGTGAAGGATCCTCCGGTTTACCGCTCCC 1080
 Db 1021 GGATCTTTCACCGCTCATCTTTATCTGTGAAGGATCCTCCGGTTTACCGCTCCC 1080
 Qy 1081 AGCAGAAGTGTGATTAACCAAGTGTGATGACCCCATCCAAAGTTTGGAAATTCGAGA 1140
 Db 1081 AGCAGAAGTGTGATTAACCAAGTGTGATGACCCCATCCAAAGTTTGGAAATTCGAGA 1140
 Qy 1141 TGAAACAAGGTGTGATTAACCAAGTGTGATGAGGAGTGGGAGTATCTTTGTTAAATGCGCCTCA 1200
 Db 1141 TGAAACAAGGTGTGATTAACCAAGTGTGATGAGGAGTGGGAGTATCTTTGTTAAATGCGCCTCA 1200
 Qy 1201 TCTCTCTCTGAAATGGCATCTTTTACTTTTCAGCTCTGCTCCAGAGGAGATTTCTTCT 1260
 Db 1201 TCTCTCTCTGAAATGGCATCTTTTACTTTTGAACCTCTGCTCCAGAGGAGATTTCTTCT 1260
 Qy 1261 CCATTCATATCCGAGCAGCAGGGAGCTGGACAGAAAAATCTATAAGGGCTTTTCGAACAAC 1320
 Db 1261 CCATTCATATCCGAGCAGCAGGGAGCTGGACAGAAAAATCTATAAGGGCTTTTCGAACAAC 1320
 Qy 1321 AATATTTCAACATTTCCAGGATTTGAATGGATGGTCCCTTTGGCAGCAGCGAGTGGAGTG 1380
 Db 1321 AATATTTCAACATTTCCAGGATTTGAATGGATGGTCCCTTTGGCAGCAGCGAGTGGAGTG 1380
 Qy 1381 TTTTTCAGTATGAAGTGGCTGTCTGTTTGGAGCAGGAATTTGGGTCACCCCTTTGCTT 1440
 Db 1381 TTTTTCAGTATGAAGTGGCTGTCTGTTTGGAGCAGGAATTTGGGTCACCCCTTTGCTT 1440
 Qy 1441 CTATCTTGAATTCATCTGGTACAAATTCAGTGTGCAGACCAACCTCAAAACAAAAA 1500
 Db 1441 CTATCTTGAATTCATCTGGTACAAATTCAGTGTGCAGACCAACCTCAAAACAAAAA 1500

Qy 1501 AGATCTATTTCTACTGGATCTGCAGGAGACAGGTGCTTTTCTGCTGCTCAACCAACCTGT 1560
 Db 1501 AGATCTATTTCTACTGGATCTGCAGGAGACAGGTGCTTTTCTGCTGCTCAACCAACCTGT 1560
 Qy 1561 TGACTTCCCTGGAAACAGGAGATGGAGAAATTTAGGCAAGTGGGTTTCTAAACTACCGTC 1620
 Db 1561 TGACTTCCCTGGAAACAGGAGATGGAGAAATTTAGGCAAGTGGGTTTCTAAACTACCGTC 1620
 Qy 1621 TCTTCTCTCACCGGATGGGACAGCAATATTTGTTGGTCATGACGCAATTTAACTTTGACAAG 1680
 Db 1621 TCTTCTCTCACCGGATGGGACAGCAATATTTGTTGGTCATGACGCAATTTAACTTTGACAAG 1680
 Qy 1681 CCATGACATCTGACAGGCTGAAACAGAAAACTCTTTTGGGAGACCAATGTTGGGACA 1740
 Db 1681 CCATGACATCTGACAGGCTGAAACAGAAAACTCTCTTTGGGAGACCAATGTTGGGACA 1740
 Qy 1741 ATGAGTTTCTCAATAGCTACCTCCCAACCAAGTCTGTAGTGGGAGTCTTTCTATGTG 1800
 Db 1741 ATGAGTTTCTCAATAGCTACCTCCCAACCAAGTCTGTAGTGGGAGTCTTTCTATGTG 1800
 Qy 1801 GCCCTCGGACTTTGGCAAGAGCCTGCGCAAAATGCTGTCAACGATATTTCCAGTCTGGATC 1860
 Db 1801 GCCCTCGGACTTTGGCAAGAGCCTGCGCAAAATGCTGTCAACGATATTTCCAGTCTGGATC 1860
 Qy 1861 CTAGAAAGTTCAAATCTTACTTCAACAAAGAAAAATTTTGGAGTTATAGGAATTAAGGACGG 1920
 Db 1861 CTAGAAAGTTCAAATCTTACTTCAACAAAGAAAAATTTTGGAGTTATAGGAATTAAGGACGG 1920
 Qy 1921 TAACTGCAATTTTCTCTTTTGTATCTTCACTAATTTAGTATATAGGAATAAGGACGGTAA 1980
 Db 1921 TAACTGCAATTTTCTCTTTTGTATCTTCACTAATTTAGTATATAGGAATAAGGACGGTAA 1980
 Qy 1981 TCTGCAATTTGCTCTTTTGTATCTTCACTAATTTACTTGGTCTCTGAGTGTGANCAGT 2040
 Db 1981 TCTGCAATTTGCTCTTTTGTATCTTCACTAATTTACTTGGTCTCTGAGTGTGANCAGT 2040
 Qy 2041 CACTTTAGGATTAAGAAATGCTCTCAAGCCTTCACTCCCTGGTATTTCTTTTGTGATG 2100
 Db 2041 CACTTTAGGATTAAGAAATGCTCTCAAGCCTTCACTCCCTGGTATTTCTTTTGTGATG 2100
 Qy 2101 CATTCAACTCTGTTTACTTGGAGCTTCAAGCACTTAAAGAACTCTTGAAGTCTTTTAAAGTCT 2160
 Db 2101 CATTCAACTCTGTTTACTTGGAGCTTCAAGCACTTAAAGAACTCTTGAAGTCTTTTAAAGTCT 2160
 Qy 2161 GAANTTTTAAAGCCCATGGATCCTTTCTCAGAAAAATAAATGTAATAATTTCTCGACAG 2220
 Db 2161 GAANTTTCTAAAGCCCATGGATCCTTTCTCAGAAAAATAAATGTAATAATTTCTCGACAG 2220
 Qy 2221 CCATGACTGTAGCAAGGCTTGATAGCAAGTTTGGTGGTTCANAAATTAACAATAATC 2280
 Db 2221 CCATGACTGTAGCAAGGCTTGATAGCAAGTTTGGTGGTTCANAAATTAACAATAATC 2280
 Qy 2281 CCAGTGAATTTTATCAATTTCCAGTGTATCCATCTCTCAGTGTGTTGTTGTTGTTGTTG 2340
 Db 2281 CCAGTGAATTTTATCAATTTCCAGTGTATCCATCTCTCAGTGTGTTGTTGTTGTTGTTG 2340
 Qy 2341 TCCCTCCCAACCCCAAGAGATTTTAAAGTGGGAGTCTTTTAAATTAATAATTTTATGGA 2400
 Db 2341 TCCCTCCCAACCCCAAGAGATTTTAAAGTGGGAGTCTTTTAAATTAATAATTTTATGGA 2400
 Qy 2401 ATAAATTAATTAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATA 2460
 Db 2401 ATAAATTAATTAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATA 2460
 Qy 2461 ATCCCAATATAACCAACAGTGTACATGTTTACTGTCACTTTTGTATGTTGTTGTTGTTG 2520
 Db 2461 ATCCCAATATAACCAACAGTGTACATGTTTACTGTCACTTTTGTATGTTGTTGTTGTTG 2520
 Qy 2521 TGTGACAGCAATTTATTTATTTTGTCTCATCAAAAAATAAAGATTTTTCACTTGAA 2580
 Db 2521 TGTGACAGCAATTTATTTATTTTGTCTCATCAAAAAATAAAGATTTTTCACTTGAA 2580

	QY	2581	AAAAAAAAAAAAA	2609	
	Dd	2581	AAAAAAAAAAAAA	2609	
	RESULT 3				
	ADAB3892				
	ID	ADA83892	standard; DNA; 2609 BP.		
	XX AC	ADA83892;			
	DT XX	20-NOV-2003	(first entry)		
	DE XX	Human NOX1 gene.			
	XX	human; marker; expressed sequence tag; EST; arabidopsis; tumour;			
	KW	stress-induced phenotype; hyperosmotic stress; colon cancer; immunogen;			
	KW	vaccine; ds; gene.			
	XX OS	Homo sapiens.			
	PN	WO2002103028-A2.			
	PD	27-DEC-2002.			
	PF	30-MAY-2002; 2002WO-IB004189.			
	XX PR	30-MAY-2001; 2001US-0293999P.			
	PR	22-OCT-2001; 2001US-0330457P.			
	XX PR	19-FEB-2002; 2002US-0357144P.			
	PA	(BIOM-) BIOMEDICAL CENT.			
	PI	Baranova AV, Yankovsky NK, Kozlov AP, Lobashev AV, Krukovskaya LL;			
	DR	WPI; 2003-175241/17.			
	XX P-PSDB; ADAB3894.				
	PT	Determining if a nucleic acid is a marker for a phenotype/cell type of interest, by global comparison of expressed sequence tags known to be expressed in the phenotype/cell type with all ESTs expressed in normal tissue.			
	XX PS	Claim 23; Page 292-294; 516pp; English.			
	CC	The invention relates to a novel method for determining if a nucleic acid is a marker for a predetermined phenotype/cell type of interest from a biological species. The method comprises performing a global comparison of a group of expressed sequence tags (ESTs) known to be expressed in the phenotype/cell type of interest with all ESTs expressed in normal tissue in order to identify ESTs that are preferentially expressed in the phenotype/cell type of interest. A method of the invention is useful for determining whether a nucleic acid is a marker for a predetermined phenotype or cell type of interest from a biological species, preferably Arabidopsis or human. The cell type of interest is an abnormal cell such as a tumour cell, and the predetermined phenotype is a stress-induced phenotype such as hyperosmotic stress or high salt conditions. A method of the invention is also useful for determining the progression of colon cancer in a human, for detecting a tumour cell, and for regulating or preventing the growth of a tumour cell. An antibody of the invention is useful for detecting the absence or presence of peptides encoded by tumour-associated markers. A polypeptide of the invention is useful as an immunogen for vaccinating an animal. The present sequence encodes a tumour-associated antigen of the invention.			
	XX	Sequence 2609 BP; 703 A; 574 C; 549 G; 779 T; 0 U; 4 Other;			
	Query Match	99.8%; Score 2605; DB 7; Length 2609;			
	Best Local Similarity	100.0%; Pred. No. 0;			
	Matches 2609; Conservative	0; Mismatches 0; Indels 0; Gaps 0;			
	QY	1	GCTGATAGCACAGTTCTGTCCACAGAAGCGGGGAATAAACTTATTTCATTCGCCAGAA	60	

QY 1141 TGAACAGCGTGGCTTCAGCATGGAAGTGGGGCAGTATATCTTTGTTAAATTGCCCTCAA 1200
 Db 1141 TGAACAGCGTGGCTTCAGCATGGAAGTGGGGCAGTATATCTTTGTTAAATTGCCCTCAA 1200
 QY 1201 TCTCTCTCCCTGGAATGGCATCTTTTACTTTTACCTCTGCTCCAGAGGAAGATTCTTCT 1260
 Db 1201 TCTCTCTCCCTGGAATGGCATCTTTTACTTTTACCTCTGCTCCAGAGGAAGATTCTTCT 1260
 QY 1261 CCATTTCATATCCGAGCAGCGGACTGGACAGAAAATCTCATAGGCGCTTCGAAACAAC 1320
 Db 1261 CCATTTCATATCCGAGCAGCGGACTGGACAGAAAATCTCATAGGCGCTTCGAAACAAC 1320
 QY 1321 AATATTCCCAATTCAGGATTCAGTGGATGCTGCTTTGGCAGCAGCGAGTGGAGTG 1380
 Db 1321 AATATTCCCAATTCAGGATTCAGTGGATGCTGCTTTGGCAGCAGCGAGTGGAGTG 1380
 QY 1381 TTTTCCAGTATGAAGTGGCTGCTGCTGGTGGAGCAGGAATGGGGTCAACCCCTTTGCTT 1440
 Db 1381 TTTTCCAGTATGAAGTGGCTGCTGCTGGTGGAGCAGGAATGGGGTCAACCCCTTTGCTT 1440
 QY 1441 CTATCTTGAATTCATCTGGTACAAAATCCAGTGTGCAGACAACAACCTCAAAAACAAAA 1500
 Db 1441 CTATCTTGAATTCATCTGGTACAAAATCCAGTGTGCAGACAACAACCTCAAAAACAAAA 1500
 QY 1501 AGATCTATTTCTACTGGATCTGCAGGGAGACAGTGGCTTTTCTGTTTCAACACCTGT 1560
 Db 1501 AGATCTATTTCTACTGGATCTGCAGGGAGACAGTGGCTTTTCTGTTTCAACACCTGT 1560
 QY 1561 TGACTTCCCTGGAACAGAGATGGAGGAATTAGGCAAGTGGGTTTTCTAAACTACCGTC 1620
 Db 1561 TGACTTCCCTGGAACAGAGATGGAGGAATTAGGCAAGTGGGTTTTCTAAACTACCGTC 1620
 QY 1621 TCTTCTCACCGGATGGAGCAGCAATATTTGTTGGTCAAGAGCAATTAACCTTGCAGAGG 1680
 Db 1621 TCTTCTCACCGGATGGAGCAGCAATATTTGTTGGTCAAGAGCAATTAACCTTGCAGAGG 1680
 QY 1681 CCACTGACATCTGCAGAGTCTGAAACAGAAAACCTCTTGGGAGCAACCAATGGGACA 1740
 Db 1681 CCACTGACATCTGCAGAGTCTGAAACAGAAAACCTCTTGGGAGCAACCAATGGGACA 1740
 QY 1741 ATGAGTTTTCTACATAGTACCTCCACCCCAAGTCTGTAGTGGGAGTTTTCTATGTG 1800
 Db 1741 ATGAGTTTTCTACATAGTACCTCCACCCCAAGTCTGTAGTGGGAGTTTTCTATGTG 1800
 QY 1801 GCCCTCGACTTTGCAAGAGCCTGCGCAAAATGCTGTCACCGATATTCAGTCTGATC 1860
 Db 1801 GCCCTCGACTTTGCAAGAGCCTGCGCAAAATGCTGTCACCGATATTCAGTCTGATC 1860
 QY 1861 CTAGAAAGGTTCAATTTCTACTTCAACAAGAAAATTTTTGAGTTATAGGAATAAGGACGG 1920
 Db 1861 CTAGAAAGGTTCAATTTCTACTTCAACAAGAAAATTTTTGAGTTATAGGAATAAGGACGG 1920
 QY 1921 TAATCTGCAATTTGCTCTTTGTATCTTCAAGTAAATGAGTTATAGGAATAAGGACGTA 1980
 Db 1921 TAATCTGCAATTTGCTCTTTGTATCTTCAAGTAAATGAGTTATAGGAATAAGGACGTA 1980
 QY 1981 TCTGCAATTTGCTCTTTGTATCTTCAAGTAAATGAGTTATAGGAATAAGGACGTA 2040
 Db 1981 TCTGCAATTTGCTCTTTGTATCTTCAAGTAAATGAGTTATAGGAATAAGGACGTA 2040
 QY 2041 CACTTTAGGATAAGAAATGCTCTCAAGCCCTGACTCCCTGGTATCTTTTTTTGATG 2100
 Db 2041 CACTTTAGGATAAGAAATGCTCTCAAGCCCTGACTCCCTGGTATCTTTTTTTGATG 2100
 QY 2101 CATTCAACTCTGTTACTTGGATCTCAGCAACTTAAAGACTCTTGAAGTCTTAAAGTCT 2160
 Db 2101 CATTCAACTCTGTTACTTGGATCTCAGCAACTTAAAGACTCTTGAAGTCTTAAAGTCT 2160
 QY 2161 GAANTTCTTAAGCCCATGGATCCCTTCTCAGAAAATAAAGTAAATCTTCTGGACAG 2220
 Db 2161 GAANTTCTTAAGCCCATGGATCCCTTCTCAGAAAATAAAGTAAATCTTCTGGACAG 2220

QY 2221 CCATGACTGTAGCAAGGCTTGATAGCAGAAAGTTTGGTGGTTCANAAATTATACAACCTAATC 2280
 Db 2221 CCATGACTGTAGCAAGGCTTGATAGCAGAAAGTTTGGTGGTTCANAAATTATACAACCTAATC 2280
 QY 2281 CCAGGTGATTTTATCAATTCAGTGTACCATTCTCCTGAGTTTTGGTTTTGTAATCTTTTG 2340
 Db 2281 CCAGGTGATTTTATCAATTCAGTGTACCATTCTCCTGAGTTTTGGTTTTGTAATCTTTTG 2340
 QY 2341 TCCCTCCACCCCCACAGAGATTTTAAAGTAGGGTGAATTTTAAATAAAAAATTATTTGA 2400
 Db 2341 TCCCTCCACCCCCACAGAGATTTTAAAGTAGGGTGAATTTTAAATAAAAAATTATTTGA 2400
 QY 2401 ATAATTATGATTAACATAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 2460
 Db 2401 ATAATTATGATTAACATAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 2460
 QY 2461 ATCCCCATATACACCAACAGTGTACATGTTTACTGTCTCTTTGATATGTTTATCCAG 2520
 Db 2461 ATCCCCATATACACCAACAGTGTACATGTTTACTGTCTCTTTGATATGTTTATCCAG 2520
 QY 2521 TGTGAACAGCAATTTATTTTGTCTCATCAAAAATAAAGGATTTTTTTCACCTTGAA 2580
 Db 2521 TGTGAACAGCAATTTATTTTGTCTCATCAAAAATAAAGGATTTTTTTCACCTTGAA 2580
 QY 2581 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2609
 Db 2581 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2609

RESULT 4
 ABK37993
 ID ABK37993 standard; DNA; 2608 BP.
 XX
 AC ABK37993;
 XX
 DT 21-MAY-2002 (first entry)
 XX
 DE Human colon specific gene (CSG) Cln106.
 XX
 KW Human; colon specific; gene; CSG; gene; ds; cytostatic; metastasis;
 colon cancer staging.
 XX
 OS Homo sapiens.
 XX
 PN WO200206515-A2.
 XX
 PD 24-JAN-2002.
 XX
 PF 17-JUL-2001; 2001WO-US022454.
 XX
 PR 17-JUL-2000; 2000US-(0618596.
 XX
 PA (DIAD-) DIADEXUS INC.
 XX
 PI Macina RA, Sun Y;
 XX
 WI WPI; 2002-171815/22.
 XX
 XX Diagnosing, staging or monitoring colon cancer involves determining a
 colon specific gene in cells, tissues or body fluids in patient, and
 comparing it with levels of the gene from a normal human control.
 XX
 Claim 7; Page 51-52; 52pp; English.
 XX
 CC The invention relates to diagnosing the presence of colon cancer,
 metastases of colon cancer, staging colon cancer, monitoring colon cancer
 for the onset of metastasis or monitoring a change in stage of colon
 cancer in a patient. The method involves determining a colon specific
 gene (CSG) in cells, tissues or bodily fluids and comparing it with
 levels of CSG in cells, tissues or bodily fluids from a normal human
 control. Colon cancer can be treated by administering a molecule which
 down regulates the expression or activity of CSG. An immune response
 against a target cell expressing CSG can be induced by delivering an

CC immunologically stimulatory amount of a CSG protein to a patient, so that
 CC an immune response is mounted. Therapeutic agents are useful for imaging
 CC colon cancer in a patient by administering an agent labelled with
 CC paramagnetic ions or a radioisotope to the patient. They are also useful
 CC for preventing the onset of colon cancer, and in diagnosis and treatment
 CC of the disease. This sequence represents a colon specific gene of the
 CC invention
 XX
 SQ Sequence 2608 BP; 703 A; 574 C; 548 G; 779 T; 0 U; 4 Other;

Query Match 99.4%; Score 2593; DB 6; Length 2608;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 2608; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY	1	GCTGATAGCAGTTCGTCCAGAGAGGAGCGGAATAAATTAATTCATCCAGGAA	60
DB	1	GCTGATAGCAGTTCGTCCAGAGAGGAGCGGAATAAATTAATTCATCCAGGAA	60
QY	61	CTCTTGGGGTAGGTGTGTTTTCATCTTAAGGCTCACAGACCTCGCTGGACAA	120
DB	61	CTCTTGGGGTAGGTGTGTTTTCATCTTAAGGCTCACAGACCTCGCTGGACAA	120
QY	121	ATGTTCCATTCCTGAAGGAGCTCTCCAGAATCCGGATTGCTGAATCTTCCCTGTGGCTA	180
DB	121	ATGTTCCATTCCTGAAGGAGCTCTCCAGAATCCGGATTGCTGAATCTTCCCTGTGGCTA	180
QY	181	GAAGGGCTCAAAACCACTCTTGACAAATGGGAACTGGGTGGTAAACCACTGGTTTCAG	240
DB	181	GAAGGGCTCAAAACCACTCTTGACAAATGGGAACTGGGTGGTAAACCACTGGTTTCAG	240
QY	241	TTTGTGTTCTGGTGTGTTGGTAGGCTGAATGTTTCTGTTGGTGGATGGCTTCCTGA	300
DB	241	TTTGTGTTCTGGTGTGTTGGTAGGCTGAATGTTTCTGTTGGTGGATGGCTTCCTGA	300
QY	301	AATATGAGAGGCGCAAAATACTACTACAAAGAAATCCCTGGGTCAACATGGCCT	360
DB	301	AATATGAGAGGCGCAAAATACTACTACAAAGAAATCCCTGGGTCAACATGGCCT	360
QY	361	GTGCCGAGGCTGCTCTCTGCTTGAATTTTAAACAGACGCTGATCCTGCTTCCTGTGT	420
DB	361	GTGCCGAGGCTGCTCTCTGCTTGAATTTTAAACAGACGCTGATCCTGCTTCCTGTGT	420
QY	421	GTGCCAATCTGCTGCTCTCTGAGGGGACCTGCTCAATTTGCGCGGACACCTGAGAA	480
DB	421	GTGCCAATCTGCTGCTCTCTGAGGGGACCTGCTCAATTTGCGCGGACACCTGAGAA	480
QY	481	AGCAATTGGATCAACACCTCACCTTCCAAAGCTGGTGGCTATATGATCTGCTACATA	540
DB	481	AGCAATTGGATCAACACCTCACCTTCCAAAGCTGGTGGCTATATGATCTGCTACATA	540
QY	541	CAGCTATTACATTCATGACACCTGTTTAACTTTGACTGCTATAGCAGAGCCGACAGG	600
DB	541	CAGCTATTACATTCATGACACCTGTTTAACTTTGACTGCTATAGCAGAGCCGACAGG	600
QY	601	CCACAGATGGCTCCCTTGGCTCCTCATCTCCAGGCTATCTCATGATGAGAAAGGGGG	660
DB	601	CCACAGATGGCTCCCTTGGCTCCTCATCTCCAGGCTATCTCATGATGAGAAAGGGGG	660
QY	661	GTTCTTGGCTAAATCCATCCAGTCCCGAAACACGACAGTGGAGTATGACATTCACCA	720
DB	661	GTTCTTGGCTAAATCCATCCAGTCCCGAAACACGACAGTGGAGTATGACATTCACCA	720
QY	721	GGTTGCTGCTCACTGGAGTGATCATGACAAATAGCCTTGATTCATGTTAACTTCAG	780
DB	721	GGTTGCTGCTCACTGGAGTGATCATGACAAATAGCCTTGATTCATGTTAACTTCAG	780
QY	781	CTACTCAGTTTCATCCGGAGGAGTATTTGAAGTCTTCTGGTATCTCACACCTTTTAA	840
DB	781	CTACTCAGTTTCATCCGGAGGAGTATTTGAAGTCTTCTGGTATCTCACACCTTTTAA	840
QY	841	TCTTCTATATCCTTGGCTTAGGGATTTCAGGCAATGGTGAATTTGCCGGGGTCAACAG	900
DB	841	TCTTCTATATCCTTGGCTTAGGGATTTCAGGCAATGGTGAATTTGCCGGGGTCAACAG	900

QY	901	AGGAGAGCATGAATGAGAGTCACTCTCGAAGTGTGCAGAGTCTTTTGAATGGGATG	960
DB	901	AGGAGAGCATGAATGAGAGTCACTCTCGAAGTGTGCAGAGTCTTTTGAATGGGATG	960
QY	961	ATCGTGACTCCCACTGTAGGCGCCCTAAGTTTGAAGGGCATCCCTCTGAGTCTTGAAGT	1020
DB	961	ATCGTGACTCCCACTGTAGGCGCCCTAAGTTTGAAGGGCATCCCTCTGAGTCTTGAAGT	1020
QY	1021	GGATCCTTGACCGGTCATCTTTATATCTGTGAAGGATCCCTCCGCTTTTACCGTCCC	1080
DB	1021	GGATCCTTGACCGGTCATCTTTATATCTGTGAAGGATCCCTCCGCTTTTACCGTCCC	1080
QY	1081	AGCAGAAGGTTGTGATTACCAAGTTTGTATGACACCATCCAAAGTTTTCGAATTGCGA	1140
DB	1081	AGCAGAAGGTTGTGATTACCAAGTTTGTATGACACCATCCAAAGTTTTCGAATTGCGA	1140
QY	1141	TGAACAAGCGTGGCTTCAGCATGGAAGTGGGGCAGTATATCTTTGTTAAATGGCCCTCAA	1200
DB	1141	TGAACAAGCGTGGCTTCAGCATGGAAGTGGGGCAGTATATCTTTGTTAAATGGCCCTCAA	1200
QY	1201	TCTCTCTCTGGAAATGCAATCTTTTACTTTTGACCTCTGCTCCAGAGGAAGATTTCTCT	1260
DB	1201	TCTCTCTCTGGAAATGCAATCTTTTACTTTTGACCTCTGCTCCAGAGGAAGATTTCTCT	1260
QY	1261	CCATTCAATATCCGAGCAGCAGGGAATCTGACAGAAAATCTATAAGGGCTTTTGAACAAC	1320
DB	1261	CCATTCAATATCCGAGCAGCAGGGAATCTGACAGAAAATCTATAAGGGCTTTTGAACAAC	1320
QY	1321	AATATTCAACAATCCAGAGTTGAAGTGGTGGTCCCTTTGGCAGCAGCAGTGGAGATG	1380
DB	1321	AATATTCAACAATCCAGAGTTGAAGTGGTGGTCCCTTTGGCAGCAGCAGTGGAGATG	1380
QY	1381	TTTTCCAGTATGAAGTGGCTGCTGCTGTTGGAGCAGGAATTCGGGTCAACCCCTTTGCTT	1440
DB	1381	TTTTCCAGTATGAAGTGGCTGCTGCTGTTGGAGCAGGAATTCGGGTCAACCCCTTTGCTT	1440
QY	1441	CTATCTTGAATCCATCTGCTACAAATCCAGTGTGCAGACCAACCAACCTCAAAACAAA	1500
DB	1441	CTATCTTGAATCCATCTGCTACAAATCCAGTGTGCAGACCAACCAACCTCAAAACAAA	1500
QY	1501	AGATCTATTTTCTAGTGGTCTGAGGAGCAGGTGCTCTTCTGCTTCAACAACCTGT	1560
DB	1501	AGATCTATTTTCTAGTGGTCTGAGGAGCAGGTGCTCTTCTGCTTCAACAACCTGT	1560
QY	1561	TGACTTCCCTGGAACAGGAGATGGAGGAATTAGGCAAGTGGTCTTCTAAACTACGTC	1620
DB	1561	TGACTTCCCTGGAACAGGAGATGGAGGAATTAGGCAAGTGGTCTTCTAAACTACGTC	1620
QY	1621	TCTTCTCACCAGTGGGACAGCAATATTTGGTCTATGCTGAGCATTAACCTTTGACAAGG	1680
DB	1621	TCTTCTCACCAGTGGGACAGCAATATTTGGTCTATGCTGAGCATTAACCTTTGACAAGG	1680
QY	1681	CCACTGACATCTGACAGGTCTGAAACAGAAACCTTCTTTGGGAGACCAATGTTGGACA	1740
DB	1681	CCACTGACATCTGACAGGTCTGAAACAGAAACCTTCTTTGGGAGACCAATGTTGGACA	1740
QY	1741	ATGAGTTTTTCTACATAGTCTACCTCCACCCCAAGTCTGAGTGGAGTCTTCTATGTG	1800
DB	1741	ATGAGTTTTTCTACATAGTCTACCTCCACCCCAAGTCTGAGTGGAGTCTTCTATGTG	1800
QY	1801	GCCCTCGGACTTTGGCAAGAGCCTGGCAATGCTGTCCAGCATATTCAGTCTGGATC	1860
DB	1801	GCCCTCGGACTTTGGCAAGAGCCTGGCAATGCTGTCCAGCATATTCAGTCTGGATC	1860
QY	1861	CTAGAAAGGTTCAATCTTCAACAAAGAAAATTTTGTAGTTATAGGAATAAGGACGG	1920
DB	1861	CTAGAAAGGTTCAATCTTCAACAAAGAAAATTTTGTAGTTATAGGAATAAGGACGG	1920
QY	1921	TAATCTGCAATTTGCTCTTCTGATCTTCAAGTATGAGTATAGGAATAAGGACGGTAA	1980
DB	1921	TAATCTGCAATTTGCTCTTCTGATCTTCAAGTATGAGTATAGGAATAAGGACGGTAA	1980

QY 1981 TCTGCATTTGCTCTTGTATCTTCTAGTAATTTACTTGTCTCCTCAGGTTTCAGCAGT 2040
 Db |||||
 QY 1981 TCTGCATTTGCTCTTGTATCTTCTAGTAATTTACTTGTCTCCTCAGGTTTCAGCAGT 2040
 Db |||||
 QY 2041 CACTTTAGGATAAGAAATGCTCTCAAGCCTTCTGACTCCCTGGTATCTTTTGTGATTG 2100
 Db |||||
 QY 2041 CACTTTA-GATAGAAATGCTCTCAAGCCTTCTGACTCCCTGGTATCTTTTGTGATTG 2099
 Db |||||
 QY 2101 CATTCAATCTGTTACTTGTAGCTTCTGAGCACTTAAAGAACTTCTGAAAGTCTTAAAGTCT 2160
 Db |||||
 QY 2100 CATTCAATCTGTTACTTGTAGCTTCTGAGCACTTAAAGAACTTCTGAAAGTCTTAAAGTCT 2159
 Db |||||
 QY 2161 GAANTTCTTAAAGCCATGGAATCTTCTCAGAAATAAATCTGTAATCTTCTGGAAG 2220
 Db |||||
 QY 2160 GAANTTCTTAAAGCCATGGAATCTTCTCAGAAATAAATCTGTAATCTTCTGGAAG 2219
 Db |||||
 QY 2221 CCATGACTGTAGCAAGGCTTGATAGCAGAAAGTTTGGTGGTTTCAAAATATATACTAATC 2280
 Db |||||
 QY 2220 CCATGACTGTAGCAAGGCTTGATAGCAGAAAGTTTGGTGGTTTCAAAATATATACTAATC 2279
 Db |||||
 QY 2281 CCAGGTGATTTTATCAATCCAGTGTACATCTCTGAGTTTGGTGGTTTCAATCTTTG 2340
 Db |||||
 QY 2280 CCAGGTGATTTTATCAATCCAGTGTACATCTCTGAGTTTGGTGGTTTCAATCTTTG 2339
 Db |||||
 QY 2341 TCCCTCCACCCACAGCAAGATTTTAAAGTGGTGGTGGTTTAAATAAATAATTTATTGA 2400
 Db |||||
 QY 2340 TCCCTCCACCCACAGCAAGATTTTAAAGTGGTGGTGGTTTAAATAAATAATTTATTGA 2399
 Db |||||
 QY 2401 ATAATTAATGATAAACAATAATAATAATAATAATAATAATAATAATAATAATAATAATA 2460
 Db |||||
 QY 2400 ATAATTAATGATAAACAATAATAATAATAATAATAATAATAATAATAATAATAATAATA 2459
 Db |||||
 QY 2461 ATCCCATATACCAACACAGTGTACATCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2520
 Db |||||
 QY 2460 ATCCCATATACCAACACAGTGTACATCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2519
 Db |||||
 QY 2521 TGTGAACAGCAATTTATTATTATTTTCTCATCAAAAAATAAAGGATTTTTTTTCACTGAA 2580
 Db |||||
 QY 2520 TGTGAACAGCAATTTATTATTATTTTCTCATCAAAAAATAAAGGATTTTTTTTCACTGAA 2579
 Db |||||
 QY 2581 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2609
 Db AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2608

RESULT 5
 ABK37991
 ID ABK37991 standard; DNA; 1881 BP.
 AC ABK37991;
 XX
 XX
 XX 21-MAY-2002 (first entry)
 DT Human colon specific gene (CSG) splice variant #1.
 DE Human; colon specific gene; CSG; gene; da; cytostatic; metastasis;
 KW colon cancer staging.
 XX Homo sapiens.
 OS
 XX WO200206515-A2.
 PN
 XX
 XX 24-JAN-2002.
 PD
 XX 17-JUL-2001; 2001WO-US022454.
 PF
 XX 17-JUL-2000; 2000US-00618596.
 PR
 XX (DIAD-) DIADEXUS INC.
 PA
 XX Macina RA, Sun Y;
 PI WPI; 2002-171815/22.
 DR

DR P-PSDB; AAU85422.
 XX
 PT Diagnosing, staging or monitoring colon cancer involves determining a
 PT colon specific gene in cells, tissues or body fluids in patient, and
 PT comparing it with levels of the gene from a normal human control.
 XX
 PS Claim 7; Page 30-31; 52pp; English.
 XX
 CC The invention relates to diagnosing the presence of colon cancer,
 CC metastases of colon cancer, staging colon cancer, monitoring colon cancer
 CC for the onset of metastasis or monitoring a change in stage of colon
 CC cancer in a patient. The method involves determining a colon specific
 CC gene (CSG) in cells, tissues or bodily fluids and comparing it with
 CC levels of CSG in cells, tissues or bodily fluids from a normal human
 CC control. Colon cancer can be treated by administering a molecule which
 CC down regulates the expression or activity of CSG. An immune response
 CC against a target cell expressing CSG can be induced by delivering an
 CC immunologically stimulatory amount of a CSG protein to a patient, so that
 CC an immune response is mounted. Therapeutic agents are useful for imaging
 CC colon cancer in a patient by administering an agent labelled with
 CC paramagnetic ions or a radioisotope to the patient. They are also useful
 CC for preventing the onset of colon cancer, and in diagnosis and treatment
 CC of the disease. This sequence represents a colon specific gene of the
 CC invention
 XX
 SQ Sequence 1881 BP; 461 A; 443 C; 434 G; 543 T; 0 U; 0 Other;
 Query Match 69.8%; Score 1820.2; DB 6; Length 1881;
 Best Local Similarity 99.8%; Pred. No. 0;
 Matches 1822; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 137 GGACCTCTCCAGATCCGATTGCTGAATCTTCCCTGTGTGCTAGAGGGCTCCAAACCA 196
 Db |||||
 QY 197 CCTCTTGACAAATGGGAACTGGGTGGTTAAACCACTGGTTTTTCAGTTTGTCTGTGTGT 256
 Db |||||
 QY 257 TTGGTAGGCTGAATGTTTCTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 316
 Db |||||
 QY 121 TTGGTAGGCTGAATGTTTCTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 180
 Db |||||
 QY 317 CAATACTACTACACAGAAATCCCTGGGTCAACATGTCCTGTGCTGCTGCTGCTGCTGCTG 376
 Db |||||
 QY 181 CAATACTACTACACAGAAATCCCTGGGTCAACATGTCCTGTGCTGCTGCTGCTGCTGCTG 240
 Db |||||
 QY 377 TCTCTGCTTGAATTTAAACAGCAGCTGATCCTGCTTCTCTGTGTGTGTGTGTGTGTGTGT 436
 Db |||||
 QY 241 TCTCTGCTTGAATTTAAACAGCAGCTGATCCTGCTTCTCTGTGTGTGTGTGTGTGTGTGT 300
 Db |||||
 QY 437 CTTCCTGAGGGGACCTGCTCATTTTGCAGCGCACACTGAGAAAGCAATTTGGATCAAA 496
 Db |||||
 QY 301 CTTCCTGAGGGGACCTGCTCATTTTGCAGCGCACACTGAGAAAGCAATTTGGATCAAA 360
 Db |||||
 QY 497 CCTCACCTTCCACAAGCTGGTGGCTATATGATCTGCTTACATACAGTATTTTCAATCAT 556
 Db |||||
 QY 361 CCTCACCTTCCACAAGCTGGTGGCTATATGATCTGCTTACATACAGTATTTTCAATCAT 420
 Db |||||
 QY 557 TGCACACCTGTTTAACTTTTGA CTGCTATAGCAGAAAGCGCAGGCGCAGATGGTCCCT 616
 Db |||||
 QY 421 TGCACACCTGTTTAACTTTTGA CTGCTATAGCAGAAAGCGCAGGCGCAGATGGTCCCT 480
 Db |||||
 QY 617 TGCCTCCATTTCTCCAGCTTCTCATGATGAGAAAGGGGGTCTTCTGCTAAATCC 676
 Db |||||
 QY 481 TGCCTCCATTTCTCCAGCTTCTCATGATGAGAAAGGGGGTCTTCTGCTAAATCC 540
 Db |||||
 QY 677 CATCCAGTCCCGAAACACAGCAGTGGAGTATGTGACATTCACACAGCTTGTGGTCTCAC 736
 Db |||||
 QY 541 CATCCAGTCCCGAAACACAGCAGTGGAGTATGTGACATTCACACAGCTTGTGGTCTCAC 600
 Db |||||
 QY 737 TGGAGTGATCATGACAAATAGCCTTGATTTCTATGTTAACTTACGTACTGATTTTATCCG 796
 Db |||||

Db 601 TGGAGTGATCATGACAAATGACCTTGATCTCATGGTAACCTTCAGCTACTGAGTTCATCCG 660
 QY 797 GAGGAGTATTTGAGTCTTTGGTATATCTCAACCTTTTATCTTCTATATCTCTTGG 856
 Db 661 GAGGAGTATTTGAGTCTTTGGTATATCTCAACCTTTTATCTTCTATATCTCTTGG 720
 QY 857 CTTTAGGATTCAGCGCATTTGGTGAATGTCGCGGGTCAACACAGAGAGACATGAATGA 916
 Db 721 CTTTAGGATTCAGCGCATTTGGTGAATGTCGCGGGTCAACACAGAGAGACATGAATGA 780
 QY 917 GAGTCATCTCGCAAGTGTGCAGAGTCTTTTGAGATGTGGATGATCGTGACTCCCACTG 976
 Db 781 GAGTCATCTCGCAAGTGTGCAGAGTCTTTTGAGATGTGGATGATCGTGACTCCCACTG 840
 QY 977 TAGCGCGCTTAAGTTTGAAGGCAATCCCTCGAGTCTTGGAAAGTGAATCTTGCACCGGT 1036
 Db 841 TAGCGCGCTTAAGTTTGAAGGCAATCCCTCGAGTCTTGGAAAGTGAATCTTGCACCGGT 900
 QY 1037 CATCTCTTATATCTGTGAAGGATCTCTCGGTGTTTACCGCTCCACAGAGAGTGTGAT 1096
 Db 901 CATCTCTTATATCTGTGAAGGATCTCTCGGTGTTTACCGCTCCACAGAGAGTGTGAT 960
 QY 1097 TACCAAGTGTGTTATGACCCATCCAAAGTTTGGAAATTCAGATGAACAAGCGTGCTT 1156
 Db 961 TACCAAGTGTGTTATGACCCATCCAAAGTTTGGAAATTCAGATGAACAAGCGTGCTT 1020
 QY 1157 CAGCATGGAAGTGGGAGTATATCTTTGTTAATGTCCTCAATCTCTCTCGTGAATG 1216
 Db 1021 CAGCATGGAAGTGGGAGTATATCTTTGTTAATGTCCTCAATCTCTCTCGTGAATG 1080
 QY 1217 GCATCTTTTACTTTCAGCTCTCTCCAGAGAGATTTCTTCCATCATATCCGAGC 1276
 Db 1081 GCATCTTTTACTTTCAGCTCTCTCCAGAGAGATTTCTTCCATCATATCCGAGC 1140
 QY 1277 AGCAGGGGACTGACAGAAATCTCATAAGGGCTTTCGAACAACAATATTCACCAATTC 1336
 Db 1141 AGCAGGGGACTGACAGAAATCTCATAAGGGCTTTCGAACAACAATATTCACCAATTC 1200
 QY 1337 CAGGATGAGTGGATGTCCTTTGGCAGACGAGTGGATGTTTTCAGTATGAAGT 1396
 Db 1201 CAGGATGAGTGGATGTCCTTTGGCAGACGAGTGGATGTTTTCAGTATGAAGT 1260
 QY 1397 GGTCTGCTGTTGGAGAGCAATTTGGGTGACCCCTTGTCTTCTATCTTGAATCCAT 1456
 Db 1261 GGTCTGCTGTTGGAGAGCAATTTGGGTGACCCCTTGTCTTCTATCTTGAATCCAT 1320
 QY 1457 CTGGTACAAATTCAGTGTGCAGACCAACCTCAAAACAAAAGATCTATTTCTACTG 1516
 Db 1321 CTGGTACAAATTCAGTGTGCAGACCAACCTCAAAACAAAAGATCTATTTCTACTG 1380
 QY 1517 GATCTCAGGGAGACAGTGGCTTTTCTGGTTCAACACCTGTTGACTTCCCTGGAACA 1576
 Db 1381 GATCTCAGGGAGACAGTGGCTTTTCTGGTTCAACACCTGTTGACTTCCCTGGAACA 1440
 QY 1577 GGAGATGGAGGAATTAGGCAAGTGGTCTTCTAAACTACCGTCTCTCTCTACCGGATG 1636
 Db 1441 GGAGATGGAGGAATTAGGCAAGTGGTCTTCTAAACTACCGTCTCTCTCTACCGGATG 1500
 QY 1637 GGACAGCAATATTTGGTTCATGACAGCAATTAACCTTTGACAGGCCACTGACATCGTGAC 1696
 Db 1501 GGACAGCAATATTTGGTTCATGACAGCAATTAACCTTTGACAGGCCACTGACATCGTGAC 1560
 QY 1697 AGTCTGAAACAGAAACCTCTTTGGGAGACCAATGTGGGCAATGAGTTTCTCAAT 1756
 Db 1561 AGTCTGAAACAGAAACCTCTTTGGGAGACCAATGTGGGCAATGAGTTTCTCAAT 1620
 QY 1757 AGTCTCTCCACCCCAAGTCTCTAGTGGAGTTTCTTATGTGGCCCTCGGACTTTGGC 1816
 Db 1621 AGTCTCTCCACCCCAAGTCTCTAGTGGAGTTTCTTATGTGGCCCTCGGACTTTGGC 1680
 QY 1817 AAAGACCTGCGCAATGTGTCAACGATATTCAGTCTGGATCTAGAAAGTTCAT 1876
 Db 1681 AAAGACCTGCGCAATGTGTCAACGATATTCAGTCTGGATCTAGAAAGTTCAT 1740

QY 1877 CTACTTCAACAAAGAAAAATTTTGGTTATAGGAATAAGACGCGTAATCTGCATTTTGC 1936
 Db 1741 CTACTTCAACAAAGAAAAATTTTGGTTATAGGAATAAGACGCGTAATCTGCATTTTGC 1800
 QY 1937 TCTTTGTATCTTCAGTAATTGAGTT 1961
 Db 1801 TCTTTGTATCTTCAGTAATTTACTT 1825

RESULT 6
 AAD00694
 ID AAD00694 standard; cDNA; 2577 BP.
 XX
 AC AAD00694;
 XX
 DT 08-SEP-2000 (first entry)
 XX
 DE Rat mitogenic regulator mox1 cDNA.
 XX
 KW Rat; mitogenic regulator; mox1; mitogenic oxidase; p65mox; superoxide;
 KW reactive oxygen intermediate; ROI; cell division; cytostatic;
 KW antipsoriatic; cardiant; antiarteriosclerotic; vasotropic;
 KW antiangiogenic; hypotensive; drug development; treatment; cancer;
 KW abnormal growth; psoriasis; prostatic hypertrophy; proliferation;
 KW blood vessel; lymphatic vessel; benign prostatic hypertrophy;
 KW cardiovascular disease; arteriovenous malformation; eye disorder;
 KW hypertension; atherosclerosis; restenosis; angioplasty; ss.
 XX
 OS Rattus sp.
 XX
 FH Key
 FT 5'UTR Location/Qualifiers
 FT 1..127
 FT /*tag= a
 FT CDS 128..1819
 FT /*tag= b
 FT /product= "Mox1"
 FT /note= "Mitogenic oxidase"
 FT 3'UTR 1820..2577
 FT /*tag= c
 FT polyA_signal 2201..2206
 FT /*tag= d
 FT polyA_signal 2550..2555
 FT /*tag= e
 PN W0200028031-A2.
 XX
 PD 18-MAY-2000.
 XX
 PF 10-NOV-1999; 99WO-US026592.
 XX
 PR 10-NOV-1998; 98US-0107911P.
 PR 17-AUG-1999; 99US-0149332P.
 PR 27-AUG-1999; 99US-0151242P.
 XX
 PA (UYEM-) UNIV EMORY.
 XX
 PI Lambeth JD, Lassegue BP, Griending KK, Arnold RS, Guangjie C;
 XX
 DR WPI: 2000-376545/32.
 DR P-PSDB; AAY71121.
 XX
 PS Protein capable of stimulating superoxide production, useful for treating
 conditions associated with abnormal growth, including cancer.
 XX
 PS Claim 4; Page 100-102; 141pp; English.
 XX
 CC The present sequence is a cDNA encoding rat mitogenic oxidase mox1, also
 referred as p65mox, which is capable of stimulating production of
 superoxide, a reactive oxygen intermediate (ROI) that affects cell
 division. The present sequence was obtained from a rat aortic smooth
 muscle cell. The mox1 protein functions as a mitogenic regulator and
 shows homology to human mox1 protein. It is expressed in aortic smooth

CC	muscle cells and induced by angiotensin II, platelet-derived growth factor (PDGF) and phorbol myristic acid (PMA). The present sequence is useful in developing drugs and therapies for treatment of conditions associated with abnormal growth, including cancer, psoriasis, prostatic hypertrophy, benign prostatic hypertrophy, cardiovascular disease, proliferation of vessels, e.g. blood vessels and lymphatic vessels, arteriovenous malformation, vascular problems associated with eye, CC atherosclerosis, hypertension, and restenosis following angioplasty	XX
SQ	Sequence 2577 BP; 690 A; 571 C; 545 G; 771 T; 0 U; 0 Other;	
	Query Match 50.0%; Score 1305; DB 3; Length 2577;	
	Best Local Similarity 83.4%; Pred. No. 1.5e-273;	
	Matches 149; Conservative 0; Mismatches 295; Indels 3; Gaps 1;	
QY	132 CTGAAGGACCTCTCCAGAATCCGGAATGCTGAATCTTCCTCTGTGCTAGAAGGGCTCCA	191
DB	53 CAGAAGTTCCTATCTCTGAAGGATCCCATCAGAGAAACGAGATTGCTCTTAAGAGGCTCCA	112
QY	192 AACCACTCTTGAAATGGGAACCTGGTGGTTAACCACTGGTTTCAGATTTGTTTCTG	251
DB	113 GACCTCATTTGACAAATGGGAACCTGGCTGGTTAAACCACCTGGCTCTCAGTTTTGTTTCTG	172
QY	252 GTTGTTTGGTTAGGCTGAATGTTTTCTCTGTTGTGTGATGCTTCCTGGAATATGAGAAG	311
DB	173 GTTCTTGGTTGGGCTGAACATTTTCTGTTGTGTACGTCTCTCTGAATTATGAGAAG	232
QY	312 GCGACAAATACTACTACACAGAAGAAATCTCTGGGTCAACATTTGGGCTGTGCCCGAGCG	371
DB	233 TCTGACAAGTACTATTACAGAGAGAAATTCCTGGAACTGCTTTGGGCTTTGGCCAGAGCA	292
QY	372 TCTGCTCTCTGCTTGAATTTTAAACAGACACGCTGATCTCTTCTCTGTGTGTCGCAATCTG	431
DB	293 TCTGCTTTGGCTCGAATTTTAAACAGACATGGTGTATCTCTGATCTCTGTGTGTCGAAATCTG	352
QY	432 CTGTCCTCTCTGAGGGGCACTGCTCATTTTGCAGCCGCACTGTAGAAAGCAATTGGAT	491
DB	353 CTCTCTCTCTGAGGGGCACCTGCTCATTTTGCACACACACGCTGAGAAAGCCATTGGAT	412
QY	492 CACAACCTCACTTCCACAGCTGGTGGCCTATATGATCTGCCTACATACAGCTATTTCAC	551
DB	413 CACAACCTCACTTCCATAGCTGGTGGCATATATGATCTGCATATTTCACAGCTATTTCAT	472
QY	552 ATCATTTGCACACCTGTTTAACTTTTGACTGTCTATAGCAGAGCCCAACAGGCCACAGATGGC	611
DB	473 ATCATTTGCACATCTATTAACTTTTGAAGCTACAGTAGAAGCCAAACAGGCCATGGATGGA	532
QY	612 TCCCTTGGCTCCATCTCTCCAGCCTATCTCATGATAGAGAAAAGGGGGGTTCTTTGGCTA	671
DB	533 TCTCTTGGCTCTGTCTCTCCAGCCTATTCCATCCCGAGAAA---GAAGATTTCTTTGGCTA	589
QY	672 AATCCCATCCAGTCCCGAAAACACACAGTGGAGTATGTGACATTCACACGCTTGTCTGGT	731
DB	590 AATCCCATCCAGTCTCCAAAGTGACAGTATGATGACAGCAATTACAGTATTTGCTGGC	649
QY	732 CTACCTGGAGTGATCATGACAAATAGCCCTTGATTCATGTGTAACCTTCAGCTATCGAGTTC	791
DB	650 CTTACTGGAGTGTGCGCACTGTGGCTTTGGTTCTCATGTGTAACCTTCAGCTATGGAGTTT	709
QY	792 ATCCGAGGAGGTTATTTTGAAGTCTCTGTGTAATCTCACACCTTTTATCTCTCTATATC	851
DB	710 ATCCGAGGAATTAATTTTGACTCTTCTGGTATACATCACCTTTTCACTCATCTATATC	769
QY	852 CTTGGCTTAGGGAATTCAGGCATTTGGTGAATTTGTCCGGGGTCAACAGAGGAGAGCATG	911
DB	770 ATCTGCTTAGGGAATCCATGGCTCGGGGGGATTTGTCCGGGGTCAACAGAGAGAGCATG	829
QY	912 AATCAGAGTCACTCTCCGAAGTGTGCAGAGTCTTTTGAGATGTGGGATGATCGTGACTCC	971
DB	830 AGTGAAGTCACTCCCGCACTGTTTCATCTCTTTCCACGATGGGATAGATGTAAGAGG	889
QY	972 CACTGTAGGGGCCCTTAAGTTTGAAGGGCATCCCCCTGAGTCTTGGAGTGGATCTTTCGCA	1031

KW Rat; mitogenic regulator; mox1B; mitogenic oxidase; p65mox; superoxide;
 KW reactive oxygen intermediate; ROI; cell division; cyostatic;
 KW antipsoriatic; cardiant; antiarteriosclerotic; vasotropic;
 KW antiangiogenic; hypotensive; drug development; treatment; cancer;
 KW abnormal growth; psoriasis; prostatic hypertrophy; proliferation;
 KW blood vessel; lymphatic vessel; benign prostatic hypertrophy;
 KW cardiovascular disease; arteriovenous malformation; eye disorder;
 KW hypertension; atherosclerosis; restenosis; angioplasty; ss.
 XX Rattus sp.
 XX
 XX Location/Qualifiers
 FH Key 362..1861
 FT CDS /*tag= a
 FT /product= "Mox1B"
 FT /note= "mitogenic oxidase"
 FT polyA_signal 2243..2248
 FT /*tag= b
 FT polyA_signal 2592..2597
 FT /*tag= c
 XX WO200028031-A2.
 XX
 XX 18-MAY-2000.
 XX
 XX 10-NOV-1999; 99WO-US026592.
 XX
 XX 10-NOV-1998; 98US-0107911P.
 PR 17-AUG-1999; 99US-0149332P.
 PR 27-AUG-1999; 99US-0151242P.
 XX
 XX (UYEM-) UNIV EMORY.
 XX
 XX Lambeth JD, Lassegue BP, Griendling KK, Arnold RS, Guangjie C;
 XX WPI; 2000-376545/32.
 DR P-PSDB; AAY71122.
 DR
 DR Protein capable of stimulating superoxide production, useful for treating
 PT conditions associated with abnormal growth, including cancer.
 PT
 XX
 XX Claim 4; Page 118-120; 141pp; English.
 XX
 XX The present sequence is a cDNA encoding rat mitogenic oxidase mox1B which
 CC is capable of stimulating production of superoxide, a reactive oxygen
 CC intermediate (ROI) that affects cell division. The present sequence was
 CC obtained from a rat cDNA library constructed in a ZAP express lambda
 CC phage vector using RNA from rat vascular smooth muscle cells exposed to
 CC angiotensin II. Mox1B is a spliced variant of rat mox1, also referred as
 CC p65mox. The mox1B protein functions as a mitogenic regulator. The present
 CC sequence is useful in developing drugs and therapies for treatment of
 CC conditions associated with abnormal growth, including cancer, psoriasis,
 CC prostatic hypertrophy, benign prostatic hypertrophy, cardiovascular
 CC disease, proliferation of vessels, e.g. blood vessels and lymphatic
 CC vessels, arteriovenous malformation, vascular problems associated with
 CC eye, atherosclerosis, hypertension, and restenosis following angioplasty
 XX
 XX Sequence 2619 BP; 692 A; 596 C; 541 G; 790 T; 0 U; 0 Other;
 SQ
 Query Match 45.3%; Score 1182.8; DB 3; Length 2619;
 Best Local Similarity 84.8%; Pred. No. 5.3e-247;
 Matches 1338; Conservative 0; Mismatches 237; Indels 3; Gaps 1;
 347 GTCACATGGCTGTGCCGACGCTGTCTCTCTGCTTGAATTTTAAACAGACGCTGAT 406
 Db 310 GACTGCTTGGCTTGGCCAGACGATCTGCTTTGTGCTGAAATTTTAAACAGATGTGAT 369
 QY 407 CTGCTCTCTGTGTGCGAATCTGCTTCTTCTGAGGGGACCTGCTCATTTTGCAG 466
 Db 370 CTGATTCCTGTGTGCGAATCTGCTCTCTTCTGAGGGGACCTGCTCATTTTGCAG 429
 QY 467 CCGCACACTGAGAAAGCAATTGGATCACACCTCACCTTCCACAGCTGTGSCCTATAT 526

Db 430 CCACGCTGAGAAAGCCATTGGATCACAACTCACTTCCATAAGCTGTGGCATATAT 489
 QY 527 GATCTGCCATACATACAGCTATTACATCATTTGACACCTGTTTAACTTTGACTGCTATAG 586
 Db 490 GATCTGCATATTACAGCTATTACATCATTTGACATCATTTTAACTTTGAAAGCTACAG 549
 QY 587 CAGAACCCAGCAGGACAGAGTGGCTCCCTTGGCTCCATCTCTCCAGCCTATCTCATGA 646
 Db 550 TAGAAGCCAAACAGGCCATGGATGCTCTTGGCTCTGTTCTCTCCAGCCTATTCCATCC 609
 QY 647 TGAGRAAAAGGGGGTCTTGGCTAAATCCATCCAGTCCGAAACACAGACAGTGGAGTA 706
 Db 610 CGAGAAA---GAGATTCTTGGCTAAATCCATCCAGTCTCCAAACGTGACGTGATGTA 666
 QY 707 TGTGACATTACCCAGCGTGTGCTGCTCACTGGAGTGATCATGACAAATAGCCTTGATTTCT 766
 Db 667 TGCAGCATTTACCAGTATTGCTGGCCTTACTGGAGTGGTCCGACCTGTGGCTTTGGTTCT 726
 QY 767 CATGTAACCTTACAGCTACTGAGTTTATCCGAGAGAGTTATTTTGAAGTCTTCTGGTATAC 826
 Db 727 CATGTAACCTTACAGCTATGAGTTTATCCGAGAGATTTATTTTGAAGTCTTCTGGTATAC 786
 QY 827 TCACCACTTTTATCTTATATCTTGGCTTAGGATTCAGGCTTGGAGTGTGGATTTGT 886
 Db 787 ACATCACCTTTTATCATCTATCATCTGCTTAGGATTCATGGCTCGGGGGGATTTGT 846
 QY 887 CCGGGTCAAAACAGAGAGAGCATGAATGAGAGTTCATCTCCAGAGTGTGACAGTCTTT 946
 Db 847 CCGGGTCAAAACAGAGAGAGCATGAGTGAAGTTCATCCCGCAACTGTTTATCATCTTT 906
 QY 947 TGAGATGTGGATGATCGTGACTCCCACTGTAGGCGCCCTAAGTTTGAAGGGGATCCCC 1006
 Db 907 CCACGAGTGGGATAAGTATGAAAGGAGTTGCGAGGAGTCTCTCAATTTTGTGGGGCAACCCC 966
 QY 1007 TGAGTCTTGGAAAGTGGATCCTTGACCGGCTCATCTTATATCTGTAAGAGATCTCCG 1066
 Db 967 TGAHCTTGGAAAGTGGATCCTCGGCGGATTCGCTTTTATATCTTGAAGAGATCTCTCG 1026
 QY 1067 GTTTTACCGCTCCACGAGAGGTTGTGATTACCAAGTGTGTTATGACCCCATCCAAAGT 1126
 Db 1027 CTTTTATCGCTCCCGCAGAGGCTGTGATACCAAGTTGTTCATGCCCATGTAAAGT 1086
 QY 1127 TTTGAAATGCGATGAACAGAGTGGCTTACGATGGAAGTGGGCGAGTATATCTTTGT 1186
 Db 1087 TTTGAAATGCGATGAGGAGCGGGCTTTACTATGGAATAGGACAGTATATTTTGT 1146
 QY 1187 TAATTCGCCCTCAATCTCTCTCTGAAATGGCATCTTTTACTTTTACCTCTGCTCCAGA 1246
 Db 1147 AAATTCGCCCTCGATTTCTTCTCTGAAATGGCATCTTTTACTTCTGACCTCTGCTCCAGA 1206
 QY 1247 GGAAGATTTCTTCTCCATTCATATCCGAGCAGCGGGAGCTGGACAGAAATCTCTAAG 1306
 Db 1207 GGAAGATTTTCTCCATTCATATTCGAGCAGCAGGGAGCTGGACAGAAATCTCTAAG 1266
 QY 1307 GCTTTGCAACACAAATATTCACCAATTCGAGGATGAAGTGGATGGTCCCTTGGCAC 1366
 Db 1267 GACATTTGAACACACGACTCCCAATGCCAGGATCGAGGTGGATGGTCCCTTGGCAC 1326
 QY 1367 AGCCAGTGGAGTGTTTTCCAGTATGAACTGCTGCTGTTGGAGCAGGAATTCGGGT 1426
 Db 1327 AGTCAGTGGAGTGTCTTCCAGTACGAGTGGCTGTACTGTTGGGCGAGGATTTGGCT 1386
 QY 1427 CACCCCTTTGCTTCTATCTTGAATTCATCTGGTACAAATTCAGTGTGACAGACACAA 1486
 Db 1387 CACTCCCTTTGCTTCTCTTCTGAAATCTATCTGTAACAAATTCAGCGTGCACACACAA 1446
 QY 1487 CTTCAAAAACAAAAGATCTATTTCTACTGGATTCGACGAGAGACAGTGGCTTTCTCTG 1546
 Db 1447 GCTGAAAACAAAAGATCTATTTCTACTGGATTTGTAGAGAGACGGGTGCTTTGCTCTG 1506
 QY 1547 GTTCAACAACCTTTGACTTCTCCGACAGAGATGGAGGAATTAGGCAAGTGGGTTT 1606
 Db 1507 GTTCAACAACCTTATTGAATTCCTGGAACAGAGATGGAGGAATTAGGCAACCGGATTT 1566

PR 08-NOV-2000; 2000US-0246528P.
 PR 08-NOV-2000; 2000US-0246532P.
 PR 08-NOV-2000; 2000US-0246609P.
 PR 08-NOV-2000; 2000US-0246610P.
 PR 08-NOV-2000; 2000US-0246611P.
 PR 08-NOV-2000; 2000US-0246613P.
 PR 17-NOV-2000; 2000US-0249207P.
 PR 17-NOV-2000; 2000US-0249208P.
 PR 17-NOV-2000; 2000US-0249209P.
 PR 17-NOV-2000; 2000US-0249210P.
 PR 17-NOV-2000; 2000US-0249211P.
 PR 17-NOV-2000; 2000US-0249212P.
 PR 17-NOV-2000; 2000US-0249213P.
 PR 17-NOV-2000; 2000US-0249214P.
 PR 17-NOV-2000; 2000US-0249215P.
 PR 17-NOV-2000; 2000US-0249216P.
 PR 17-NOV-2000; 2000US-0249217P.
 PR 17-NOV-2000; 2000US-0249218P.
 PR 17-NOV-2000; 2000US-0249244P.
 PR 17-NOV-2000; 2000US-0249245P.
 PR 17-NOV-2000; 2000US-0249264P.
 PR 17-NOV-2000; 2000US-0249265P.
 PR 17-NOV-2000; 2000US-0249297P.
 PR 17-NOV-2000; 2000US-0249299P.
 PR 17-NOV-2000; 2000US-0249300P.
 PR 01-DEC-2000; 2000US-0250160P.
 PR 01-DEC-2000; 2000US-0250391P.
 PR 05-DEC-2000; 2000US-0251030P.
 PR 05-DEC-2000; 2000US-0251988P.
 PR 05-DEC-2000; 2000US-0256719P.
 PR 06-DEC-2000; 2000US-0251479P.
 PR 08-DEC-2000; 2000US-0251856P.
 PR 08-DEC-2000; 2000US-0251868P.
 PR 08-DEC-2000; 2000US-0251869P.
 PR 08-DEC-2000; 2000US-0251989P.
 PR 08-DEC-2000; 2000US-0251990P.
 PR 11-DEC-2000; 2000US-0254037P.
 PR 05-JAN-2001; 2001US-0259678P.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 XX
 PI Rosen CA, Barash SC, Ruben SM;
 XX
 XX WPI; 2001-502630/55.
 DR
 XX Polynucleotides encoding digestive system antigens, useful for
 PT diagnosing, treating, preventing and/or prognosing disorders of the
 PT digestive system, particularly cancer and cancer metastases.
 XX
 PS Disclosure; SEQ ID NO 2637; 986pp; English.
 XX
 CC The present invention provides the protein and coding sequences of a
 CC number of human digestive system antigens. These can be used in the
 CC diagnosis, treatment and prevention of digestive system disorders,
 CC including cancer, Meckel's diverticulum, bacterial or parasitic
 CC infections, appendicitis, Hirschsprung's disease, chronic colitis or
 CC ulcerative colitis. The present sequence is a genomic DNA fragment
 CC encoding a digestive system antigen of the invention
 XX
 XX Sequence 7517 BP; 2203 A; 1530 C; 1735 G; 2049 T; 0 U; 0 Other;
 SQ
 Query Match 24.2%; Score 630.6; DB 4; Length 7517;
 Best Local Similarity 91.3%; Pred. No. 7.1e-127;
 Matches 735; Conservative 0; Mismatches 8; Indels 62; Gaps 4;
 QY 1772 CAAAGTCTGTAGTGGAGTTTCTTATGTGCGCCCTCGACCTTTCGCAAGAGCCTGCGCAA 1831
 DB 6261 CAGGTCTGTAGTGGAGTTTCTTATGTGCGCCCTCGACCTTTCGCAAGAGCCTGCGCAA 6320
 QY 1832 ATGCTGTACCGATATCCAGTCTGGATCTAGAAAGTTTCAATTCTTACTTCAACAAAGA 1891
 DB 6321 ATGCTGTACCGATATCCAGTCTGGATCTAGAAAGTTTCAATTCTTACTTCAACAAAGA 6380

QY 1892 AAATTTTGGAGTTATAGGAATAAGGACGGTAATCTGCATTTTGTCTCTTTGTATCTTCAG 1951
 DB 6381 AAATTT----- 6386
 QY 1952 TAATTGAGTTATAGGAATAAGGACGGTAATCTGCATTTTGTCTCTTTGTATCTTCAGTAA 2011
 DB 6387 ----TTGAGTTATAGGAATAAGGACGGTAATCTGCATTTTGTCTCTTTGTATCTTCAGTAA 6443
 QY 2012 TTTACTTGGTCTCNCNTCAGGTTTGANCAGTCACTTTAGGATAAGAAATGTGCTCTCAAGCC 2071
 DB 6444 TTTACTTGGTCTCGTCAGGTTTGAGCAGTCACTTTAGGATAAGAAATGTGCTCTCAAGCC 6503
 QY 2072 TTGACTCCCTGGTATCTTTTTTTTGGATTCGATTAACCTTCGTTTACTTTGAGCTTCAGCAAC 2131
 DB 6504 TTGACTCCCTGGTATCTTTTTTTTGGATTCGATTAACCTTCGTTTACTTTGAGCTTCAGCAAC 6563
 QY 2132 TTTAAGAACTTCTGAAAGTTCTTAAAGTTCTGAAGTTCTTAAAGCCCATGATCTTTCTCA 2191
 DB 6564 TTTAAGAACTTCTGAAGTTCTTAAAGTTCTGAAGTTCTTAAAGCCCATGATCTTTCTCA 6623
 QY 2192 GAAAAATACTGTAATCTTTCTGGACAGCCATGACTGTAGCAAGGCTTTGATAGCAGAAG 2251
 DB 6624 GAAAAATACTGTAATCTTTCTGGACAGCCATGACTGTAGCAAGGCTTTGATAGCAGAAG 6683
 QY 2252 TTTGGTGGTTCCANAATTATACAACTTAATCCAGGTGATTTTATCAATTCAGTGTACCA 2311
 DB 6684 TTTGGTGGTTCCAGAGTTATACAACTTAATCCAGGTGATTTTATCAATTCAGTGTACCA 6743
 QY 2312 TCTCTCGAGTTTGGTTGTGTAATCTTTGTCTCCACCCACACAGAGATTT-TAAGT 2370
 DB 6744 TCTCTCGAGTTTGGTTGTGTAATCTTTGTCTCCACCCACACAGAGATTTCTAAGT 6803
 QY 2371 AGGGTGACTTTTTAAATAAAAAATTTATTGAATAAATTAATGATAAAACATAATAATAACA 2430
 DB 6804 AGGGTGACTTTTTAAATAAAAAATTTATTGAATAAATTAATGATAAAACATAATAATAACA 6863
 QY 2431 TAAATAATAACAAATTAACGAGAACCCCATCCCATTAACACCAACAGTGTACATGT 2490
 DB 6864 TAAATAATAACAAATTAACGAGAACCCCATCCCATTAACACCAACAGTGTACATGT 6923
 QY 2491 TTACTGTCACTTTTGTATATGGT-TTATCCAGTGTGAACAGCAATTTA---TTATTTTTCG 2546
 DB 6924 TTACTGTCACTTTTGTATATGGT-TTATCCAGTGTGAACAGCAATTTTATTTTATTTTTCG 6983
 QY 2547 TCATCAAAAAATAAGGATTTTTT 2571
 DB 6984 TCATCAAAAAATAAGGATTTTCTT 7008
 RESULT 9
 AAK87743
 ID AAK87743 standard; cDNA; 1192 BP.
 XX
 AC AAK87743;
 XX
 DT 05-NOV-2001 (first entry)
 XX
 DE Human digestive system antigen coding sequence SEQ ID NO: 59.
 XX
 KW Human; digestive system antigen; gene therapy; cancer; appendicitis;
 KW ulcerative colitis; infection; Hirschsprung's disease; chronic colitis;
 KW digestive system disorder; Meckel's diverticulum; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200155314-A2.
 XX
 XX 02-AUG-2001.
 XX
 XX 17-JAN-2001; 2001WO-US001324.
 XX
 XX 31-JAN-2000; 2000US-0179065P.
 PR 04-FEB-2000; 2000US-0180628P.

PR 24-FEB-2000; 2000US-0184664P.
 PR 02-MAR-2000; 2000US-0186350P.
 PR 16-MAR-2000; 2000US-0189874P.
 PR 17-MAR-2000; 2000US-0190076P.
 PR 18-APR-2000; 2000US-01981123P.
 PR 19-MAY-2000; 2000US-0205515P.
 PR 07-JUN-2000; 2000US-0209467P.
 PR 28-JUN-2000; 2000US-0214886P.
 PR 30-JUN-2000; 2000US-0215135P.
 PR 07-JUL-2000; 2000US-0216647P.
 PR 07-JUL-2000; 2000US-0216880P.
 PR 11-JUL-2000; 2000US-0217487P.
 PR 11-JUL-2000; 2000US-0217496P.
 PR 14-JUL-2000; 2000US-0218290P.
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 PR 26-JUL-2000; 2000US-0220964P.
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 PR 14-AUG-2000; 2000US-0224519P.
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 PR 14-AUG-2000; 2000US-0225214P.
 PR 14-AUG-2000; 2000US-0225266P.
 PR 14-AUG-2000; 2000US-0225267P.
 PR 14-AUG-2000; 2000US-0225268P.
 PR 14-AUG-2000; 2000US-0225270P.
 PR 14-AUG-2000; 2000US-0225447P.
 PR 14-AUG-2000; 2000US-0225757P.
 PR 14-AUG-2000; 2000US-0225758P.
 PR 14-AUG-2000; 2000US-0225759P.
 PR 18-AUG-2000; 2000US-0226279P.
 PR 22-AUG-2000; 2000US-0226681P.
 PR 22-AUG-2000; 2000US-0226686P.
 PR 22-AUG-2000; 2000US-0227182P.
 PR 23-AUG-2000; 2000US-0227009P.
 PR 30-AUG-2000; 2000US-0228924P.
 PR 01-SEP-2000; 2000US-0229287P.
 PR 01-SEP-2000; 2000US-0229343P.
 PR 01-SEP-2000; 2000US-0229344P.
 PR 01-SEP-2000; 2000US-0229345P.
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 PR 05-SEP-2000; 2000US-0229513P.
 PR 06-SEP-2000; 2000US-0230437P.
 PR 06-SEP-2000; 2000US-0230438P.
 PR 08-SEP-2000; 2000US-0231242P.
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 PR 08-SEP-2000; 2000US-0231244P.
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 PR 08-SEP-2000; 2000US-0231414P.
 PR 08-SEP-2000; 2000US-0232080P.
 PR 08-SEP-2000; 2000US-0232081P.
 PR 12-SEP-2000; 2000US-0231968P.
 PR 14-SEP-2000; 2000US-0232397P.
 PR 14-SEP-2000; 2000US-0232398P.
 PR 14-SEP-2000; 2000US-0232399P.
 PR 14-SEP-2000; 2000US-0232400P.
 PR 14-SEP-2000; 2000US-0232401P.
 PR 14-SEP-2000; 2000US-0233063P.
 PR 14-SEP-2000; 2000US-0233064P.
 PR 14-SEP-2000; 2000US-0233065P.
 PR 21-SEP-2000; 2000US-0234223P.
 PR 21-SEP-2000; 2000US-0234274P.
 PR 23-SEP-2000; 2000US-0234997P.
 PR 25-SEP-2000; 2000US-0234998P.
 PR 26-SEP-2000; 2000US-0235484P.
 PR 27-SEP-2000; 2000US-0235834P.
 PR 27-SEP-2000; 2000US-0235836P.
 PR 29-SEP-2000; 2000US-0236327P.
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 PR 29-SEP-2000; 2000US-0236368P.
 PR 29-SEP-2000; 2000US-0236369P.
 PR 29-SEP-2000; 2000US-0236370P.
 PR 02-OCT-2000; 2000US-0236802P.
 PR 02-OCT-2000; 2000US-0237037P.
 PR 02-OCT-2000; 2000US-0237038P.

PR 02-OCT-2000; 2000US-0237039P.
 PR 02-OCT-2000; 2000US-0237040P.
 PR 13-OCT-2000; 2000US-0239935P.
 PR 13-OCT-2000; 2000US-0239937P.
 PR 20-OCT-2000; 2000US-0240960P.
 PR 20-OCT-2000; 2000US-0241221P.
 PR 20-OCT-2000; 2000US-0241785P.
 PR 20-OCT-2000; 2000US-0241786P.
 PR 20-OCT-2000; 2000US-0241787P.
 PR 20-OCT-2000; 2000US-0241808P.
 PR 20-OCT-2000; 2000US-0241809P.
 PR 01-NOV-2000; 2000US-0241826P.
 PR 01-NOV-2000; 2000US-0244617P.
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 PR 08-NOV-2000; 2000US-0246475P.
 PR 08-NOV-2000; 2000US-0246476P.
 PR 08-NOV-2000; 2000US-0246477P.
 PR 08-NOV-2000; 2000US-0246478P.
 PR 08-NOV-2000; 2000US-0246523P.
 PR 08-NOV-2000; 2000US-0246524P.
 PR 08-NOV-2000; 2000US-0246525P.
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 PR 08-NOV-2000; 2000US-0246527P.
 PR 08-NOV-2000; 2000US-0246528P.
 PR 08-NOV-2000; 2000US-0246532P.
 PR 08-NOV-2000; 2000US-0246609P.
 PR 08-NOV-2000; 2000US-0246610P.
 PR 08-NOV-2000; 2000US-0246611P.
 PR 08-NOV-2000; 2000US-0246613P.
 PR 17-NOV-2000; 2000US-0249207P.
 PR 17-NOV-2000; 2000US-0249208P.
 PR 17-NOV-2000; 2000US-0249209P.
 PR 17-NOV-2000; 2000US-0249210P.
 PR 17-NOV-2000; 2000US-0249211P.
 PR 17-NOV-2000; 2000US-0249212P.
 PR 17-NOV-2000; 2000US-0249213P.
 PR 17-NOV-2000; 2000US-0249214P.
 PR 17-NOV-2000; 2000US-0249218P.
 PR 17-NOV-2000; 2000US-0249244P.
 PR 17-NOV-2000; 2000US-0249245P.
 PR 17-NOV-2000; 2000US-0249246P.
 PR 17-NOV-2000; 2000US-0249259P.
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 PR 17-NOV-2000; 2000US-0249299P.
 PR 17-NOV-2000; 2000US-0249300P.
 PR 01-DEC-2000; 2000US-0250160P.
 PR 01-DEC-2000; 2000US-0250391P.
 PR 05-DEC-2000; 2000US-0251030P.
 PR 05-DEC-2000; 2000US-0251988P.
 PR 06-DEC-2000; 2000US-0256719P.
 PR 06-DEC-2000; 2000US-0251479P.
 PR 08-DEC-2000; 2000US-0251856P.
 PR 08-DEC-2000; 2000US-0251868P.
 PR 08-DEC-2000; 2000US-0251869P.
 PR 08-DEC-2000; 2000US-0251989P.
 PR 11-DEC-2000; 2000US-0254097P.
 PR 05-JAN-2001; 2001US-0259678P.

(HUMA-) HUMAN GENOME SCI INC.

Rosen CA, Barash SC, Ruben SM;

WPI; 2001-502630/55.

P-PSDB; AAM91970.

PT Polynucleotides encoding digestive system antigens, useful for
 PT diagnosing, treating, preventing and/or prognosing disorders of the
 PT digestive system, particularly cancer and cancer metastases.
 XX

Qy	564	CTGTTTAACTTTGACTGCTATAGCAGAACCGCAGCAGGCCACAGATGGCTCCCTTGCCCTCC	623	Qy	1623	TTCCCTCACCAGTGGACAGCAATATTGTTGGTTCATGCAGCATTAACCTTTGACAGGCC	1682
Db	372	CTATTTTAAATGGAATGGTGTGTGAATGCGAGTCAATAATCTGATCTCTTATTCAGTA	431	Db	1449	TACCTCACTGCTGGGATGAGTCTCAGGCCAATCACTTTGCTGTCACCATGATGAGGAG	1508
Qy	624	ATTCTCTCCAGCCTATCTCATGATGAGAAAAAGGGGGTCTTGCTGCTAAATCCCATCCAG	683	Qy	1683	ACTGACATCGTCACAGGTCTGAACAGAAAAACCTCTTTTGGGAGACCAATATGGGACAAAT	1742
Db	432	GCATCTCTGAACTTGGAGACAGGCAAAATGAAAGTTATCTCAATTTTGCTCGAAAGAGA	491	Db	1509	AAAGATGTGATCACAGGCTGAAACAAAAGACTTTGTATGGACGCCCACTGGGATAAT	1568
Qy	684	TCCCGAAACACGACAGTGG---AGTATGTGACATTCACAGCGTGTGCTCACTGGA	740	Qy	1743	GAGTTTTCTACATAGTACTCCACCCCAAGTCTGTAGTGGAGTTTTCTTATGTGGC	1802
Db	492	ATAAAGAACCCCTGAAGGAGGCTGTACCTGGCTGTGACCTGTGGCAGGCAATCACTGGA	551	Db	1569	GAATTCAGACATTTGCAAGTCAACACCCCTAAATACAGAAATAGAGTCTTCTCTGTGGA	1628
Qy	741	GTGATCATGACAATAGCTTATCTCATGTGTAATCTTACAGTACTGAGTTCAATCGGAGG	800	Qy	1803	CCTCGGACTTTGGCAAGAGCCTCGCAAAATGCTGCACCGATATTCAGTCTGGATCCT	1862
Db	552	GTGTGTCATGCGCTGTGCTCATATTAATTAATCACTTCTCTCCACCAAAACCATCGGAGG	611	Db	1629	CCTGAAAGCTTTGGCTGAAACCCCTGAGTAACAAAAGCATCTCCAATCTGAGTCTGGCCCT	1688
Qy	801	AGTTATTTTGAAGTCTCTGCTGATACACACACCTTTTATCTTCTATATCTTGGGTTA	860	Qy	1863	AGAAAGGTTCATTTCTACTTCAACAAAAGAAAAATTTTTCAGTTAT	1906
Db	612	TCTTACTTTGAAGTCTTTTGGTACACACATCATCTCTTTGTGATCTTCTTCATTTGGCCTT	671	Db	1689	CGGGAGTGCAATTTTCAATTTTCAACAGGAAAACTTCTAACTTGT	1732
Qy	861	GGGATTCAGGCATTTGGTGAATTTGTCGGGGTCAACAGAGGAGAGCATGAATGAGAGT	920	RESULT 11			
Db	672	GCCATCATGAGCTGAACGAATTTGTAAGTGGCAGACCGCAGAGAGTTTGGCTGTGCAT	731	AAS94941			
Qy	921	CATCCTCGCAAGTGTGCAGAGTCTTTTGAGATGTGGGATGATCGTACTCCACCTGTAGG	980	ID AAS94941	standard; DNA; 4324 BP.		
Db	732	AATATACAGTTTGTGAACAAAAATCTCAGAAATGGGAAAAATAA---GGAATGCCCA	788	XX AAS94941;			
Qy	981	CGCCCTAAGTTTGAAGGCACTCCGCCCTGAGTCTTTGGAAGTGGATCCTTGCAACCGCTCAT	1040	AC AAS94941;			
Db	789	ATCCCTCAGTTTGTGGAACCTCTCTATGATTTGGAATGATAGTGGTCCCATGTTT	848	XX 14-FEB-2002 (first entry)			
Qy	1041	CTTTATATCTGGAAGATCCTCGGTTTACCGCTCCCAAGCAGAGGTTGTGATTACC	1100	XX Human DNA sequence #196 expressed during foam cell differentiation.			
Db	849	CTGTATCTCTGAGAGTTTGTGCGGTTTGTGGGATCTCAACAGAGGTTGTTCATCACC	908	XX Human; foam cell differentiation; atherosclerosis; cerebral stroke;			
Qy	1101	AAGGTGTGTATGCACCCATCAAAAGTTTGGAAATTTGCAGATGAACAAGCGTGGCTCAGC	1160	XX cardiovascular disorder; coronary artery disease; gene therapy; ds.			
Db	909	AAGGTGTCTACTCACCTTTCAAAACCATCGAGTACAGATGAAGAAGGGTTCAAA	968	XX Homo sapiens.			
Qy	1161	ATGGAAGTGGGCAATATCTTTTAAATTTGCCCTCAATCTCTCTCTGGAATGGCAT	1220	XX WO200177389-A2.			
Db	969	ATGGAAGTGGGCAATATCTTTTGTCAAGTGGCCAAAGGTTTCAAGCTGGAGTGGCAC	1028	XX 18-OCT-2001.			
Qy	1221	CTTTTACTTGACCTCTGCTCCAGAGGAAGATTCTTCTCCATTCATATCCGAGCAGCA	1280	XX 04-APR-2001; 2001WO-US011128.			
Db	1029	CTTTTACTGACATCGCCCTCTGAGGAAGACTTCTTTAGTATCCATATCCGATCGTT	1088	XX 05-APR-2000; 2000US-C195106P.			
Qy	1281	GGGACTGGACAGAAATCTCATAGGGCTTTTCG-----AACACAA	1322	XX (INCY-) INCYTE GENOMICS INC.			
Db	1089	GGGACTGGACAGAGGGCTGTTCAATGCTTGTGGTGTGATAGCAGGAGTTTCAAGAT	1148	XX Shiffman D, Somogyi R, Lawn R, Seilhamer JJ, Porter GJ, Mikita T;			
Qy	1323	TATTCACAAATTCACGAGTTGAAGTGGATGGTCCCTTTGGCAGAGGAGGATGTT	1382	XX Tai J;			
Db	1149	CGGTGGAACCTACCTAAGATAGCGGTTGATGGGCCCTTTGACACTGCCAGTGAAGATGTG	1208	XX WPI; 2002-010925/01.			
Qy	1383	TTCCAGTATGAGTGGCTGCTGTTGGAGCAGGAATGGGGTCAACCCCTTTGCTTCT	1442	XX Composition useful for diagnosis of conditions, disorders or diseases			
Db	1209	TTACAGTATGAGTGGTGTATTTAGTGGAGCAGGGATTTGGGTTCACACCCCTTCGCATCC	1268	XX associated with atherosclerosis, comprises several polynucleotides that			
Qy	1443	ATCTTGAATCCATCTGTTCAAAATTCAGTGTGCAGACCAACCACTCAAAACAAAAAG	1502	XX are differentially expressed in foam cell development.			
Db	1269	ATTCTCAAGTCAAGTCTGTAACAATATTGCAATAACGCCACCATCTGAAGCTCAAAAG	1328	XX Claim 1; Page 247-248; 315pp; English.			
Qy	1503	ATCTATTTCTACTGATCTGAGGAGACAGGTCCTTTTCTGGTTCACAACTGTTG	1562	XX The present inventor relates to the isolation of human polynucleotide			
Db	1329	ATCTACTTCTACTGGCTGTGCGGGACACACATGCTTTGAGTGGTTTTCAGATCTGCTG	1388	XX sequences that are differentially expressed during foam cell			
Qy	1563	ACTTCCCTGGAACAGGAGATGGAGGAATTAGGCAAGTGGGTTTCTTAACTACCGTCTC	1622	XX differentiation. The polynucleotide sequences of the invention or a			
Db	1389	CAACTGCTGGAGACCATGACAGGAAGGAACAATGCCGCTCTCTCAGCTACACATC	1448	XX composition comprising these polynucleotides are useful as a high			
				XX throughput method for detecting altered expression of one or more			
				XX polynucleotides in a sample. The polynucleotides can be used in the			
				XX diagnosis of disorders associated with foam cell development such as			
				XX atherosclerosis, cerebral stroke, and cardiovascular disorders such as			
				XX coronary artery disease. The polynucleotide sequences can also be used			
				XX as PCR primers and probes. The polynucleotides of the invention are also			
				XX useful in gene therapy. AAS94746-AAS95021 represent the human			
				XX polynucleotide sequences of the invention which are differentially			
				XX expressed during foam cell differentiation			
				XX Sequence 4324 BP; 1268 A; 843 C; 925 G; 1286 T; 0 U; 2 Other;			

[illegible]

PF 03-OCT-2001; 2001WO-US030821.
 XX 03-OCT-2000; 2000US-0237189P.
 PR (GENE-) GENE LOGIC INC.
 XX Beazer-Barclay Y, Weissman SM, Yamaga S, Vockley J;
 PI WPI; 2002-435328/46.
 XX
 PT Detecting granulocyte activation by detecting differential expression of
 PT genes associated with granulocyte activation, which serves as diagnostic
 PT markers that is useful for monitoring disease states and drug toxicity.
 XX
 PS Claim 1; SEQ ID NO 1072; 114pp; English.
 XX
 CC The invention relates to detecting (M1) granulocyte (GC) activation
 CC (GCA), by detecting the level of expression of gene(s) (Gs) identified by
 CC DNA chip analysis as given in the specification, and comparing the
 CC expression level to an expression level in an unactivated GC, where
 CC differential expression of Gs is indicative of GCA. Also included are
 CC modulating (M2) GA by contacting GC with an agent that alters the
 CC expression of at least one gene in Gs; (2) screening (M3) for an agent
 CC capable of modulating GCA or an inflammation (especially chronic) in a
 CC tissue, an allergic response in a subject, exposure of a subject to a
 CC pathogen or sterile inflammatory disease using the gene expression
 CC profile; (3) detecting (M4) an inflammation (especially chronic) in a
 CC tissue, an allergic response in a subject, exposure of a subject to a
 CC pathogen or sterile inflammatory disease, by detecting the level of
 CC expression in a sample of the tissue of gene(s) from Gs, where the level
 CC of expression of the gene is indicative of inflammation; (4) treating
 CC (M5) an inflammation (especially chronic) or in a tissue, an allergic
 CC response in a subject, exposure of a subject to a pathogen or sterile
 CC inflammatory disease, by contacting a tissue having inflammation with an
 CC agent that modulates the expression of gene(s) from Gs in the tissue. M1
 CC is useful for detecting GCA; M2 is useful for modulating GA; M3 is useful
 CC for screening an agent capable of modulating GCA preferably in an
 CC inflammation in a tissue; M4 is useful for detecting an inflammation
 CC (especially chronic) in a tissue, an allergic response in a subject,
 CC exposure of a subject to a pathogen or sterile inflammatory disease (e.g.
 CC psoriasis, rheumatoid arthritis, glomerulonephritis, asthma, thrombosis,
 CC cardiac reperfusion injury, renal refluxion injury, ARDS, adult
 CC respiratory distress syndrome, inflammatory bowel disease, Crohn's
 CC disease, ulcerative colitis, periodontal disease; also bacterial
 CC infection, viral infection, parasitic infection, protozoal infection,
 CC fungal infection and W5 is useful for treating one of the above
 CC conditions. The present sequence represents a gene differentially
 CC expressed in granulocytes. Note: The sequence data for this patent did
 CC not form part of the printed specification, but was obtained in
 CC electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 4267 BP; 1242 A; 838 C; 913 G; 1274 T; 0 U; 0 Other;

Query Match 22.2%; Score 579.4; DB 6; Length 4267;
 Best Local Similarity 60.0%; Pred. No. 8.1e-116;
 Matches 1033; Conservative 0; Mismatches 666; Indels 24; Gaps 3;

QY 205 CAATGGAACTGGGTGTTAAACACCTGGTTTCAGTTTGTCTGTTGGTTGGTTAG 264
 DB 14 CATCGGGAACTGGGTGTTAAATGAGGGGCTCTCCATTTGTCTGTTGGTTGG 73
 QY 265 GGCTGAATGTTTCCTGTTTGTGGAATGCTTCTGGAATATGAGAGCGCGACAAATAC 324
 DB 74 GGTGGAACGTCCTCTCTGTTGTTACCGGGTTTATGATATTCACCTAAGTTCT 133
 QY 325 ACTACACAGAAAAATCCTTGGGTCAACATTTGGCTGTGCGCGAGGCTCTGCTCTCTGCT 384
 DB 134 TTTACACAGAAAAATCCTTGGGTCAACATTTGGCTGTGCGCGAGGCTCTGCTCTCTGCT 193
 QY 385 TGAATTTTACACAGCGCTGATCCTGCTTCTGTTGTTGCGAATCTGCTCTCTCTCTGA 444
 DB 194 TGAATTTTCAACTGCTGATCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 253

QY 445 GGGGCACCTGCTCATTTTGGCAGCGGCACACTGAGAAAAGCAATTTGGATCACAACCTCACCT 504
 DB 254 GGGGTTCCAGTGCCTGCTGCTCAACAAGAGTTTGAAGAGCAACTGACAGGAATCTCACCT 313
 QY 505 TCCACAGCTGGTGGCTTATGATCTGCTTACATACAGCTATTTCAATCATTTGACACACC 564
 DB 314 TTTATAAAATGGTGGCATGATGATCTTCACTCTGGGATTCACACCAATTCACATC 373
 QY 565 TGTTAACTTTGACTGCTATAGCAGAACCGACAGGCCACAGATGGCTCCCTTCCTCCA 624
 DB 374 TATTTATGTTGAATGTTGTTGAATGCCCGAGTCAATAATTTCTGATCTTTTACAGTAG 433
 QY 625 TTTCTTCCAGCTTATCTCATGATGAGAAAAGGGGGTCTTTGGCTAAAATCCCATCCAGT 684
 DB 434 CACTCTCTGAACCTTGGAGACAGGCAAAATGAAAGTTATCTCAATTTTGTCTCGAAAGAA 493
 QY 685 CCCGAAACACGACAGTGG---AGTATGTGACATTCACACAGCGTGTGCTGCTCACTGGAG 741
 DB 494 TAAAGAACCTTGAAGAGGCGCTGTACTGCTGCTGTGACCCCTGTGGCAGGCACTACTGGAG 553
 QY 742 TGATCATGACAATAGCCTTGAATCTCTCATGTGTAATTCAGCTACTGAGTTTCATCCGGAGGA 801
 DB 554 TTGTCATACGCTGTGCTCATATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 613
 QY 802 GTTATTTGAAGTCTTCTGCTATACCTACACACCTTTTATCTTCTATATCTTGGCTTAG 861
 DB 614 CTTACTTTGAAGTCTTTTGGTACACACATCATCTCTTTGTGATCTTCTTCAATTTGGCTTG 673
 QY 862 GGATTCACGGCATTTGGTGAATTTGTCGGGGTCAAAACAGAGGAGAGCATGAATGAGATC 921
 DB 674 CCATCCATGAGCTGAACGAATTTGAGTGGGAGAGCCGAGAGAGTTTGGCTGTGATTA 733
 QY 922 ATCCTCGCAAGTGTGCAGAGTCTTTTGAATGTGGGATGATCGTGAATCTCCACTGTAGGC 981
 DB 734 ATATAACAGTTTGTGAACAAAAAATCTCAGATGGGGAAAAATAA---GGAATGCCAA 790
 QY 982 GCCTTAAGTTTGAAGGCGATCCCGCTGAGTCTTTGGAAGTGGATCTTGGACCGGTCAATC 1041
 DB 791 TCCTCAGTTTGTGGAAACCCCTCTATGATCTTGGAAATGGATAGTGGGTCCCATGTTTC 850
 QY 1042 TTTATATCTGTGAAGGATCCTCGGTTTACCGTCTCCAGCAGAGAGGTTGTGATTACCA 1101
 DB 851 TGTATCTGTGAGAGTTGGTGGGTTTGGCGATCTCAACAGAGGTTGCTCATACCA 910
 QY 1102 AGTTGTTATGCAACCATCAAAAGTTTGGAAATGCAAGATGAACAAGCGTGGCTTCAGCA 1161
 DB 911 AGGTGTTCACTACCCCTTTCAAAACCATCGAGCTACAGATGAAGAAGAGGGGTTCAAAA 970
 QY 1162 TGAAGTGGGCGAGTATCTTTGTTAAATGCGCCCTCAATCTCTCTCTGGAATGGATC 1221
 DB 971 TGAAGTGGGACAAATACATTTTGTCAAGTGGCCCAAGGTTGTCAAGCTGGAGTGGCACC 1030
 QY 1222 CTTTAACTTTGACCTCTGCTCCAGAGGAAGATTTCTTCCATTCATATCCGAGCAGCAG 1281
 DB 1031 CTTTAACTTGAATCATCGCCCTTGAAGAGACTTCTTTAGTATCCATATCCGATCGTTG 1090
 QY 1282 GGAAGTGGACAGAAAATCTCAATAGGGCTTTGCG---AACAACAAT 1323
 DB 1091 GGAAGTGGACAGAGGGGCTGTTCAATGCTGTGGCTGTGATAAGCAGGAGGTTTCAAGATG 1150
 QY 1324 ATTCACCAATTC---CAGGATTTGAAGTGGTGGTCTTGGCAGACGCGAGTGGAGTGT 1383
 DB 1151 CGTGGAACTACCTAAGATAGCGGTTGATGGGCGCTTTGGCACTGCGCAGTGAAGATGTGT 1210
 QY 1384 TCCAGTATGAAGTGGCTGCTGTTGGAGCAGGAATTTGGGGTCAACCCCTTTGCTTCTA 1443
 DB 1211 TCAGCTATGAGGTGGTATGTTAGTGGAGCAGGATTTGGGGTCAACCCCTTCGATCCA 1270
 QY 1444 TCTTGAATTCATCTGGTACAAATTCAGATGTGCGACCAACACCTCAAAACAAAAAGA 1503
 DB 1271 TTCTCAAGTCAGTCTGGTACAAATATTGCAATTAACGCCCAATCTGAACTCAAAAAGA 1330

QY 1504 TCTATTCTACTGGATCTGAGGACAGGAGCTGCTTTCTGCTGTTCAACAACCTGTGA 1563
Db 1331 TCTACTTCTACTGGCTGTGCGGGACACACATCCCTTTGAGTGGTTTGAGATCTGCTGC 1390
QY 1564 CTTCCCTGGAACAGGAGATGGAGAAATTAGGCAAGTGGGTTTCTTAAACTACCGTCTCT 1623
Db 1391 AACTGCTGGAGAGCCAGATGCGAAGAGNACATGCCGGCTTCTCAGGTACAACATCT 1450
QY 1624 TCCTCCCGGATGGGACAGCAATATTGTTGGTCAATGAGCATTAATACTTTGACAAGGCCA 1683
Db 1451 ACCTCACTGGCTGGAGTGTCTCAGGCCAATCACTTTGCTGTCACCATGATGAGGAGA 1510
QY 1684 CTGACATCTGACAGTCTGAACAGAAACCTCTTTGGGACCAATGTGGACAATG 1743
Db 1511 AGATGTGATCAGAGCCCTGAACAAAGAGACTTTGTATGACGCCCAACTGGGATAATG 1570
QY 1744 AGTTTCTCAATPAGTACTCTCCACCCCAAGTCTGTAGTGGGAGTTTCTTATGTGGCC 1803
Db 1571 AATTCAAGACAATTGCAAGTCAACACCCCTAATACAGATAGAGTTTCTCTGTGGAC 1630
QY 1804 CTGGACTTTGGCAAGAGCTGCGCAATGTCTGTCACCGATATTCAGTCTGGATCTTA 1863
Db 1631 CTGAAGCCTTGGTGAAACCCCTGAGTAAACAAAGCATCTCCAACTCTGAGTCTGGCCCTC 1690
QY 1864 GAAAGTTTCAATTTACTTCAACAGAAAGAAATTTTGTAGTTAT 1906
Db 1691 GGGAGTGCTTTCATTTTCAACAGGAAACTTCTAATCTGT 1733

RESULT 13
ABK37992

ID ABK37992 standard; DNA; 658 BP.

XX AC ABK37992;

XX 21-MAY-2002 (first entry)

XX Human colon specific gene (CSG) splice variant #2.

XX Human; colon specific gene; CSG; gene; ds; cytostatic; metastasis;
XX colon cancer staging.

XX Homo sapiens.

XX WO200206515-A2.

XX 24-JAN-2002.

XX 17-JUL-2001; 2001WO-US022454.

XX 17-JUL-2000; 2000US-00618596.

XX (DIAD-) DIADEXUS INC.

XX Macina RA, Sun Y;

XX WPI; 2002-171815/22.

XX P-PSDB; AAU85423.

XX Diagnosing, staging or monitoring colon cancer involves determining a
XX colon specific gene in cells, tissues or body fluids in patient, and
XX comparing it with levels of the gene from a normal human control.

XX Claim 7; Page 31; 52pp; English.

XX The invention relates to diagnosing the presence of colon cancer.
XX metastases of colon cancer, staging colon cancer, monitoring colon cancer
XX for the onset of metastasis or monitoring a change in stage of colon
XX cancer in a patient. The method involves determining a colon specific
XX gene (CSG) in cells, tissues or bodily fluids and comparing it with
XX levels of CSG in cells, tissues or bodily fluids from a normal human
XX control. Colon cancer can be treated by administering a molecule which
XX down regulates the expression or activity of CSG. An immune response

CC against a target cell expressing CSG can be induced by delivering an
CC immunologically stimulatory amount of a CSG protein to a patient, so that
CC an immune response is mounted. Therapeutic agents are useful for imaging
CC colon cancer in a patient by administering an agent labelled with
CC paramagnetic ions or a radioisotope to the patient. They are also useful
CC for preventing the onset of colon cancer, and in diagnosis and treatment
CC of the disease. This sequence represents a colon specific gene of the
CC invention

XX Sequence 658 BP; 159 A; 168 C; 133 G; 198 T; 0 U; 0 Other;

Query Match 21.1%; Score 551.6; DB 6; Length 658;

Best Local Similarity 97.6%; Pred. No. 5.4e-110;

Matches 560; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

QY 137 GGACCTCTCCAGAAATCCGGAATGCTGAATCTTCCCTGTTGGCTAGAGGGCTCAAAACCA 196

Db 1 GGACCTCTCCAGAAATCCGGAATGCTGAATCTTCCCTGTTGGCTAGAGGGCTCAAAACCA 60

QY 197 CTTCTTGAACAATGGGAAACTGGGTGGTTAAACCACTGGTTTTCAGTTTTCGTTGT 256

Db 61 CTTCTTGAACAATGGGAAACTGGGTGGTTAAACCACTGGTTTTCAGTTTTCGTTGT 120

QY 257 TTGGTTAGGGCTGAATGTTTTCCTGTTTGTGGATGCTTCTGAAATATGAGAGGCCCA 316

Db 121 TTGGTTAGGGCTGAATGTTTTCCTGTTTGTGGATGCTTCTGAAATATGAGAGGCCCA 180

QY 317 CAAATACTACTACAAAGAAATAATCCTTGGGTCAACATTTGGCTGTGCCGAGCGTCTGC 376

Db 181 CAAATACTACTACAAAGAAATAATCCTTGGGTCAACATTTGGCTGTGCCGAGCGTCTGC 240

QY 377 TCTCTGCTTGAATTTTAAACAGCAAGCTGATCTCTGTTTCTGTTGTCGCAATCTGCTGC 436

Db 241 TCTCTGCTTGAATTTTAAACAGCAAGCTGATCTCTGTTTCTGTTGTCGCAATCTGCTGC 300

QY 437 CTTCTGAGGGGCACCTGCTCATTTTGCAGCGCGCACACTGAGAAAGCAATTGGATCACA 496

Db 301 CTTCTGAGGGGCACCTGCTCATTTTGCAGCGCGCACACTGAGAAAGCAATTGGATCACA 360

QY 497 CTTCACTTTCCACAAGCTGGTGGCTTATATGATCTGCCCTACATACAGCTATTTCACATCAT 556

Db 361 CTTCACTTTCCACAAGCTGGTGGCTTATATGATCTGCCCTACATACAGCTATTTCACATCAT 420

QY 557 TGCACACCTGTTTAACTTTGACTGTCTATAGCAGAGCCGACAGCCACAGATGGCTCCCT 616

Db 421 TGCACACCTGTTTAACTTTGACTGTCTATAGCAGAGCCGACAGCCACAGATGGCTCCCT 480

QY 617 TGCCTCCATTCTCCAGCCTATCTCATGATCAGAAAGAGGGGGTCTTGGCTAAATCC 676

Db 481 TGCCTCCATTCTCCAGCCTATCTCATGATCAGAAAGAGGGGGTCTTGGCTAAATCC 540

QY 677 CATCCAGTCCCGAAACACGACAGTGGAGTATGTG 710

Db 541 CATCCATCCCATATAACACCAACAGTGATCATG 574

RESULT 14

ADA83893

ID ADA83893 standard; DNA; 658 BP.

XX AC ADA83893;

XX 20-NOV-2003 (first entry)

XX Human NOX1 gene.

XX human; marker; expressed sequence tag; EST; arabadopsis; tumour;

XX stress-induced phenotype; hyperosmotic stress; colon cancer; immunogen;

XX vaccine; ds; gene.

XX Homo sapiens.

XX WO2002103028-A2.

XX PD 27-DEC-2002.
XX PF 30-MAY-2002; 2002WO-IB004189.
XX PR 30-MAY-2001; 2001US-0293999P.
XX PR 22-OCT-2001; 2001US-0330457P.
XX PR 19-FEB-2002; 2002US-0357144P.
XX PA (BIOM-) BIOMEDICAL CENT.
XX PI Baranova AV, Yankovsky NK, Kozlov AP, Lobashev AV, Krukovskaya LL;
XX WPI; 2003-175241/17.
XX DR P-PSDB; ADAB3895.
XX

Determining if a nucleic acid is a marker for a phenotype/cell type of interest, by global comparison of expressed sequence tags known to be expressed in the phenotype/cell type with all ESTs expressed in normal tissue.

Claim 23; Page 294; 516pp; English.

The invention relates to a novel method for determining if a nucleic acid is a marker for a predetermined phenotype/cell type of interest from a biological species. The method comprises performing a global comparison of a group of expressed sequence tags (ESTs) known to be expressed in the phenotype/cell type of interest with all ESTs expressed in normal tissue in order to identify ESTs that are preferentially expressed in the phenotype/cell type of interest. A method of the invention is useful for determining whether a nucleic acid is a marker for a predetermined phenotype or cell type of interest from a biological species, preferably Arabidopsis or human. The cell type of interest is an abnormal cell such as a tumour cell, and the predetermined phenotype is a stress-induced phenotype such as hyperosmotic stress or high salt conditions. A method of the invention is also useful for determining the progression of colon cancer in a human, for detecting a tumour cell, and for regulating or preventing the growth of a tumour cell. An antibody of the invention is useful for detecting the absence or presence of peptides encoded by tumour-associated markers. A polypeptide of the invention is useful as an immunogen for vaccinating an animal. The present sequence encodes a tumour-associated antigen of the invention.

SQ Sequence 658 BP; 159 A; 168 C; 133 G; 198 T; 0 U; 0 Other;

Query Match 21.1%; Score 551.6; DB 7; Length 658;
Best Local Similarity 97.6%; Pred. No. 5.4e-110;
Matches 560; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

QY 137 GGACCTCTCCAGATCCGGATTGCTGAATCTTCCCTGTGCTAGAGGGCTCCAAACCA 196
Db 1 GGACCTCTCCAGATCCGGATTGCTGAATCTTCCCTGTGCTAGAGGGCTCCAAACCA 60

QY 197 CCTCTTGACAAATGGGAACTGGGTGGTTAAACCACTGGTTTTTCAGTTTGTCTGGTTGT 256
Db 61 CCTCTTGACAAATGGGAACTGGGTGGTTAAACCACTGGTTTTTCAGTTTGTCTGGTTGT 120

QY 257 TTGGTTAGGCTGAATGTTTTCCTGTTTGTGGATGCCTTCTGAAATATGAGAGGCCGA 316
Db 121 TTGGTTAGGCTGAATGTTTTCCTGTTTGTGGATGCCTTCTGAAATATGAGAGGCCGA 180

QY 317 CAATACTACTACAGAAATAATCCCTTGGGTCAACATTTGGCTGTGCCGAGCGTCTGC 376
Db 181 CAATACTACTACAGAAATAATCCCTTGGGTCAACATTTGGCTGTGCCGAGCGTCTGC 240

QY 377 TCTCTGTGTAATTTTAAACAGACGCTGATCCTGCTTCTGTTGTGCGCAATCTGCTGC 436
Db 241 TCTCTGTGTAATTTTAAACAGACGCTGATCCTGCTTCTGTTGTGCGCAATCTGCTGC 300

QY 437 CTTCCTGAGGGGACCTGCTCATTTTGCAGCGGCACACTGGAAGCAATTGGATCAAA 496
Db 301 CTTCCTGAGGGGACCTGCTCATTTTGCAGCGGCACACTGGAAGCAATTGGATCAAA 360

QY 497 CCTCACCTTCCACAAGCTGGTGGCCTATATGATCTGCTACATACAGCTATTTCATCAT 556
Db 361 CCTCACCTTCCACAAGCTGGTGGCCTATATGATCTGCTACATACAGCTATTTCATCAT 420

QY 557 TGCACACCTGTTTAACTTTGACTGTATAGCAGAAGCCGACAGGCCACAGATGGCTCCCT 616
Db 421 TGCACACCTGTTTAACTTTGACTGTATAGCAGAAGCCGACAGGCCACAGATGGCTCCCT 480

QY 617 TGCTCCATTCTCTCCAGCCTATCTCATGATGAGAAAAAGGGGGTCTTTGGCTAAATCC 676
Db 481 TGCTCCATTCTCTCCAGCCTATCTCATGATGAGAAAAAGGGGGTCTTTGGCTAAATCC 540

QY 677 CATCCAGTCCGAAACAGACAGTGGAGTATGG 710
Db 541 CATCCATCCCATATATAACACACAGGTACATG 574

RESULT 15
AAD00693
ID AAD00693 standard; cDNA; 2044 BP.
XX AC
XX AAD00693;
XX DT 08-SEP-2000 (first entry)
XX DE Human mitogenic regulator mox2 cDNA.
XX KW Human; mitogenic regulator; mox2; mitogenic oxidase; superoxide;
KW reactive oxygen intermediate; ROI; cell division; cytostatic;
KW antiproliferative; cardiant; antiarteriosclerotic; vasotropic;
KW antiangiogenic; hypotensive; drug development; treatment; cancer;
KW abnormal growth; psoriasis; prostatic hypertrophy; proliferation;
KW blood vessel; lymphatic vessel; benign prostatic hypertrophy;
KW cardiovascular disease; arteriovenous malformation; eye disorder;
KW hypertension; atherosclerosis; restenosis; angioplasty; ss.
XX OS Homo sapiens.
XX FH Key Location/Qualifiers
FT CDS 104..1810
FT FT /*tag= a
FT FT /product= "Mox2"
FT FT /note= "mitogenic oxidase"
XX PN WO200028031-A2.
XX PD 18-MAY-2000.
XX PF 10-NOV-1999; 99WO-US026592.
XX PR 10-NOV-1998; 98US-0107911P.
XX PR 17-AUG-1999; 99US-0149332P.
XX PR 27-AUG-1999; 99US-0151242P.
XX PA (UYEM-) UNIV EMORY.
XX PI Lambeth JD, Lassegue BP, Griendling KK, Arnold RS, Guangjie C;
XX WPI; 2000-376545/32.
XX DR P-PSDB; AAY71120.
XX

Protein capable of stimulating superoxide production, useful for treating conditions associated with abnormal growth, including cancer.

Claim 4; Page 85-89; 141pp; English.

The present sequence is a cDNA encoding human mitogenic oxidase mox2 which is capable of stimulating production of superoxide, a reactive oxygen intermediate (ROI) that affects cell division. The present sequence was obtained by 5' and 3' RACE techniques using a human foetal kidney cDNA library. The mox2 protein functions as a mitogenic regulator and shows homology to gp91phox protein. It is primarily expressed in foetal tissues with highest expression in foetal kidney. Level of

CC expression is low in adult tissues. The present sequence is useful in
 CC developing drugs and therapies for treatment of conditions associated
 CC with abnormal growth, including cancer, psoriasis, prostatic hypertrophy,
 CC benign prostatic hypertrophy, cardiovascular disease, proliferation of
 CC vessels, e.g. blood vessels and lymphatic vessels, arteriovenous
 CC malformation, vascular problems associated with eye, atherosclerosis,
 CC hypertension, and restenosis following angioplasty
 XX
 SQ Sequence 2044 BP; 540 A; 502 C; 476 G; 526 T; 0 U; 0 Other;

Query Match 20.0%; Score 521.2; DB 3; Length 2044;
Best Local Similarity 57.4%; Pred. No. 3e-103;
Matches 1012; Conservative 0; Mismatches 723; Indels 27; Gaps 3;

Qy	202	TGACAATGGGAAACTGGGTGGTTAAACACATGGGTTTTCAGTTTGTCTCGTTGTGTGGT 261
Db	102	TCATGATGGGGTGTCTGATTTTGAATGAGGGTCTCTCCACAATATTAGTACTCTCATGGC 161
Qy	262	TAGGGCTGAATGTTTTCCTGCTTTGTGATGCGTTTCTGAAATATGAGAAGCGCACAAAT 321
Db	162	TGGGAATAAATTTTTATCTGTTTATTGACAGGTTCTACTGTTATGAAGAGGAGGATCTT 221
Qy	322	ACTACTACAAGAAAAATCCTTGGGTCAACATTTGGCCTGTGCGCGAGCGTCTGCTCTCT 381
Db	222	TCCATTACACACAGATTATTTTGGGTTTCAACACTGGCTTGGGACGAGCATCCGACTGT 281
Qy	382	GCTTGAATTTTAAACAGCACGCTGATCTGCTTCTGCTGTGTCGCAATCTGCTGTCCTTC 441
Db	282	GCTTGAATTTTAACTGTCATGCTAATTTCTAATACCTGTCAGTCGAAACCTTATTTCATCA 341
Qy	442	TGAGGGCACCTGCTCATTTTTCAGSCGCGACACTGAGAAAACAAATTGGATCACAACCTCA 501
Db	342	TAAGAGAAACAAGTATTTTGTCTGACAGAGACCGTGGAGGAGCAATTAGACAAAACCTCA 401
Qy	502	CCTTCCACAAGCTGGTGGCCTATATGATTCGCCTACATACAGCTATTTCACATATTGCAC 561
Db	402	GATTTTCAAACTGGTGCCTATGGGATAGCTGTAAATGCAACCATCCACATCGTGGCGC 461
Qy	562	ACCTGTTTAACTTTGACTGCTATTAGCAGAAGCCGACAGGCCACACAGATGGCTCCCTGCCCT 621
Db	462	ATTTCTTCACTTGGAAACGTACCACTGGAGCCAGTCCGAGGAGGCCCGAGACTTCTGG 521
Qy	622	CCATTCTCCAGCCTATCTCATGATGAGAAAAAGGGGGTTCTTGGCTAAATCCCATCC 681
Db	522	CCGCACCTTTCCAACTGGGCAACACCCCTTAACGAGAG-----CTACCTCAACCCCTGTCC 575
Qy	682	AGTCCCGAAACACACAGTGGAGTATGTGACATTCACAGCGTGTGCTCTCACTGGAG 741
Db	576	GGACCTTCCCAACAAACACACACTGAATTGCTAAGGACAAATAGCAGGGTACCGGTC 635
Qy	742	TGATCATGACAAATAGCCTTGATTCCTATGGTAACTTCAGCTACTGAGTTTCATCCGAGGA 801
Db	636	TGGTGATCTCTCTGGCTTTAGCTTTGATCATGACCTCGTCAACTGAGTTTCATCAGACAGG 695
Qy	802	GTTATTTTGAAGTCTTCTGCTATACTCACACCTTTTATCTTCTATATCCTTGGCTTAG 861
Db	696	CCTCTATAGTTGTTTCTCGTATACACACCATGTTTTTCATGCTCTCTTTCTCAGCCTGG 755
Qy	862	GGATTACGCGCATTTGGTGAATTTGCCGGGCTCAACACAGAGGAGAGCATGAATGAGAGTC 921
Db	756	CCATCCATGGACGGGTCSGATTTGTCAGGCCAAACCCCAAGACAGTCTCTCTCTGCACA 815
Qy	922	ATCCTCCGAGTGTGCAGATCTTTTGAGATGTGGGATGATCTGTGACTCCGACTGTAGGC 981
Db	816	ACATCACCTTCTGTAGAGACCGCTATCGAAGATGG---CAGACAGTGGCCCAATGCCCGC 872
Qy	982	GCCCTAAGTTTGAAGGGCATCCCCCTGAGTCTTGGAAATGGATCCTTGGACCGGTCAATC 1041
Db	873	TGCTCTCAATTTCTGGCAAGAAACCTTCGCTGCTTGGAAATGGATTTTAGGCCCTGTGCT 932
Qy	1042	TTTATATCTGTGAAGGATCTCCCGTTTTTACCCGCTCCGACGAGAAGTTGTGATTACCA 1101
Db	933	TGATGCACTTGTGAAGAATAATATAGGTTTGTGGCAATTTCAACAAGAAGTTGTCAATTACCA 992

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Job time : 1018 secs

Qy	1102	AGTTGTTATGCAACCAATCCAAAGTTTGGAAATGCGATGAACAAGCGTGGCTTCAGCA	1161
Db	993	AGTGTGTAAGCCACCCCTCTGGAGTCTCTGAACTTCACATGA AAAACGCTGGCTTTAAAA	1052
Qy	1162	TGCAAGTGGGGCAGTATATCTTTGTTAAATTGCCCCCTCAATCTCTCTCTGSAATGGCATC	1221
Db	1053	TGGGCCAGGGCAGTACATCTTGTCAGTGCACGCCATATCTTCGCTGGATGGCACC	1112
Qy	1222	CTTTATCTTTGACCTCTGCTCCAGAGGAAGATTCTTCTCCATTCAATCCGAGCAGCAG	1281
Db	1113	CCTTCAACCTTTACTCTGCCCCCAGGAAGACTTTTTCAGCGTGCAATCCGGGCACAG	1172
Qy	1282	GGCACTGGACAGAAAATCTCATAGGGCTTT-----CGAACCAAT	1323
Db	1173	GAGACTGGACAGAGCGCTACTGGAGGCTTTTGGGCGAGGGACAGGCCCTCCAGGAGC	1232
Qy	1324	ATTCAACAATTCCAGGATTTGAAGTGGATGGTCCCTTTGGCACAGCCAGTGGAGATGTTT	1383
Db	1233	CCTGGAGCCTGCCAAGCTGGCAGTGGACGGGCCCTTTGGAACTGCCCTGACAGATGAT	1292
Qy	1384	TCCAGTATGAAGTGGCTGTGCTGGTGGAGCAGAAATGGGGTCAACCCCTTTGCTTCTA	1443
Db	1293	TTCACTACCCAGTGTGTGTGTGGCTTGCOCGGGGATCGGAGTCACTCCCTTCGCTGCTC	1352
Qy	1444	TCCTGAAATCCATCTGGTACAAATTCAGTGTGCAGACCAACCTCAAAACAAAAGA	1503
Db	1353	TTCTGAAATCTATATGGTACAAATGCAGTGAGGCACAGACCCCACTCAACCTGAGCAAG	1412
Qy	1504	TCTATTTCTACTGGATCTGCAGGGAGCAGGTGCCTTTTCCCTGGTCAACAACTGTTGA	1563
Db	1413	TGTATTTCTACTGGATTTGCGGGATGCAAGAGCTTTTGAGTGGTTTGCTGATCTCTTAC	1472
Qy	1564	CTTCCCTGGAAACAGGAGATGGAGAAATTAGCAAAAGTGGGTTTTCTAAAATCAACGCTCT	1623
Db	1473	TCTCCCTGGAAACAGGATGAGTGAGCGGGGAAACTCACTTTCTGAGTTATCAATAT	1532
Qy	1624	TCCTCACCGGATGGGACAGCAATATTGTTGGTCAATGCAGCATTTAAACTTTGACAAAGCCA	1683
Db	1533	TTCTTACCGGCTGGGATGAAATCAGGCTCTTCACATAGCTTTTACACTGGGACGAAAATA	1592
Qy	1684	CTGACATCTGCAGAGTCTGAAACAGAAAACCTCCCTTTGGGAGACCAATGTGGGACAATG	1743
Db	1593	CTGACGTGATTCAGGCTTTAAGCACAAGAACCTTCTATGGGAGGCCCACTGGAAACAATG	1652
Qy	1744	AGTTTTCTACAATAGTACTCCACCCCAAGTCTGTAGTGGGAGTTTTCTTATGTGGCC	1803
Db	1653	AGTTCAAGCAGATTGCCTACAATCACCCACAGCAGCATTTGGCGTGTCTTCTGTGGAC	1712
Qy	1804	CTCGACTTTGGCAAGAGCCTGGCANAATGCTGTCTACCGAATATTCAGTCTGGATCCCTA	1863
Db	1713	CTAAAGCTCTCTCGAGACACTTCAAAAGATGTGCCACTTGTATTCATCAGCTGACCCCA	1772
Qy	1864	GAAGAAGTTCAATTTCTACTTCAACAAGAAAATTTTGTAGTTATAGGAATTAAGGACGGTAA	1923
Db	1773	GAGGTGTTCAATTTCTATTACAACAGGAGAGCTTCTAGACTTTGGAGGTCAAGTCCAGGC	1832
Qy	1924	TC TGCAATTTTGTCTCTTTGTAT	1945
Db	1833	ATTGTGTTTTCAATCAAGTTAT	1854

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Maximum Match 100%
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SUMMARIES

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7	66.8	2.6	3453	4	US-09-437-568A-47
8	65	2.5	5494	4	US-09-437-568A-45
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10	53.8	2.1	832	4	US-09-621-976-2813
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15	51	2.0	6326	4	US-10-204-708-57
16	51	2.0	7304	4	US-10-204-708-44
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22	50.2	1.9	11049	4	US-10-204-708-24
23	50	1.9	640681	4	US-09-790-988-1
24	49.2	1.9	396	4	US-09-640-173-10
25	49.2	1.9	396	4	US-09-713-550-10
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28 48.8 1.9 2116 4 US-08-635-552A-1 Sequence 1, Appli
29 48.8 1.9 3736 2 US-08-480-473B-1 Sequence 1, Appli
30 48.8 1.9 3736 3 US-08-915-213-1 Sequence 1, Appli
31 48.8 1.9 3736 3 US-09-148-547-1 Sequence 1, Appli
32 48.8 1.9 3736 3 US-09-235-217-1 Sequence 1, Appli
33 48.8 1.9 3736 4 US-09-383-581-1 Sequence 1, Appli
34 48.8 1.9 3736 5 PCT-US96-10251-1 Sequence 1, Appli
35 48.8 1.9 4055 4 US-09-620-312D-706 Sequence 706, App
36 48.8 1.9 5152 4 US-10-204-708-48 Sequence 48, Appl
37 48.4 1.9 5501 4 US-10-204-708-38 Sequence 38, Appl
38 48.2 1.8 239 4 US-09-621-976-16632 Sequence 16632, A
39 48 1.8 1937 4 US-09-647-143-1 Sequence 1, Appli
40 47.8 1.8 5562 4 US-10-204-708-63 Sequence 63, Appli
41 47.8 1.8 11131 4 US-10-204-708-27 Sequence 27, Appli
42 47.6 1.8 554 4 US-09-696-169A-14 Sequence 14, Appli
43 47.4 1.8 296 2 US-09-032-684-13 Sequence 13, Appli
44 47.4 1.8 296 4 US-09-644-460-13 Sequence 13, Appli
45 47.4 1.8 1883 4 US-09-149-476-170 Sequence 170, App

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ALIGNMENTS

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RESULT 1
US-09-437-568A-1
; Sequence 1, Application US/09437568A
; Patent No. 6620603
; GENERAL INFORMATION:
; APPLICANT: Lambeth, J. David
; APPLICANT: Griending, Kathy
; APPLICANT: Lassegue, Bernard
; APPLICANT: Arnold, Rebecca S.
; APPLICANT: Cheng, Guangjie
; TITLE OF INVENTION: No. 6620603el Mitogenic Regulators
; FILE REFERENCE: 05501-0103
; CURRENT APPLICATION NUMBER: US/09/437,568A
; CURRENT FILING DATE: 1999-11-10
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 1
; LENGTH: 2609
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (2025)
; OTHER INFORMATION: n at position 2025 = any nucleotide
; NAME/KEY: modified_base
; LOCATION: (2036)
; OTHER INFORMATION: n at position 2036 = any nucleotide
; NAME/KEY: modified_base
; LOCATION: (2164)
; OTHER INFORMATION: n at position 2164 = any nucleotide
; NAME/KEY: modified_base
; LOCATION: (2264)
; OTHER INFORMATION: n at position 2264 = any nucleotide
; NAME/KEY: CDS
; LOCATION: (207) .. (1901)
US-09-437-568A-1

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Query Match 99.8%; Score 2605; DB 4; Length 2609;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2609; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 GCTGTAGCACAGTCTGTGCCAGAGAGGCGGGAATAAACTTATTCATTCACGGAA 60
    |||||
QY 61 CTCCTGGGGTAGGTGTGTGTCTTTTTCACATCTTTAAAGGCTCACAGACCCCTGCCTGCACAA 120
    |||||
Db 61 CTCCTGGGGTAGGTGTGTGTCTTTTTCACATCTTTAAAGGCTCACAGACCCCTGCCTGCACAA 120
    |||||
QY 121 ATGTTCCATCTCTGAAGGACCTCTCCAGAAATCCGATTCCTGTAATCTTCCTGTTGCCCTA 180
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[illegible]

Qy	2341	TCCCTCCACCC	CCACAGCAAGATTTTAAGTAGGGTGACTTTTTAAATAAAAAATTTATTGA	2400
Db	2341	TCCCTCCACCC	CCACAGCAAGATTTTAAGTAGGGTGACTTTTTAAATAAAAAATTTATTGA	2400
Qy	2401	ATAATTATGATA	TAACCATATATAAACATATAAACAATAAATAACCAAAATTCGGAGAACCCC	2460
Db	2401	ATAATTATGAT	TAACCATATATAAACATATAAACAATAAATAACCAAAATTCGGAGAACCCC	2460
Qy	2461	ATCCCCATATA	CACCAACAGCTACATGTTTACTGTCACTTTTGTATATGGTTTATCCAG	2520
Db	2461	ATCCCCATATA	CACCAACAGCTACATGTTTACTGTCACTTTTGTATATGGTTTATCCAG	2520
Qy	2521	TGTGAACAGCA	ATTATTTATTTTTCCTCATCAAAAAATAAAGGATTTTTTTTCACTTGAA	2580
Db	2521	TGTGAACAGCA	ATTATTTATTTTTCCTCATCAAAAAATAAAGGATTTTTTTTCACTTGAA	2580
Qy	2581	AAAAAAAAAAAA	AAAAAAAAAAAAAAAAAAAAA	2609
Db	2581	AAAAAAAAAAAA	AAAAAAAAAAAAAAAAAAAAA	2609

RESULT 2

US-09-437-568A-22

; Sequence 22, Application US/09437568A

; Patent No. 6620603

; GENERAL INFORMATION:

; APPLICANT: Lambeth, J. David

; APPLICANT: Griendling, Kathy

; APPLICANT: Lassegue, Bernard

; APPLICANT: Arnold, Rebecca S.

; APPLICANT: Cheng, Guangjie

; TITLE OF INVENTION: No. 6620603el Mitogenic Regulators

; FILE REFERENCE: 05501-0103

; CURRENT APPLICATION NUMBER: US/09/437,568A

; CURRENT FILING DATE: 1999-11-10

; NUMBER OF SEQ ID NOS: 61

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 22

; LENGTH: 2577

; TYPE: DNA

; ORGANISM: Rat

US-09-437-568A-22

Query Match	50.0%;	Score 1305;	DB 4;	Length 2577;
Best Local Similarity	83.4%;	Pred. No. 0;		
Matches 1495;	Conservative 0;	Mismatches 295;	Indels 3;	Gaps 1;
QY	132	CTGAGGACCTCTCCAGAAATCGGATTGCTGGAATCTTCCTGTGTGCTAGAAAGGCTCCA	191	
Db	53	CAGAAGTTCTATCTCTGAAGGATCCCATCAGAGAAACGAGATTGCTCTTAAGAGGCTCCA	112	
QY	192	AACCACCTCTTGACAATGGGAAACTGGTGGTTAAACCACTGGTTTCAGTTTTGTTCGTG	251	
Db	113	GACCTCATTGACAATGGGAAACTGGCTGGTTAAACCACTGGCTCAGTTTTGTTCGTG	172	
QY	252	GTGTCTTGGTTAGGGCTGAATGTTTCCTCTTTGTGGAATCCCTCTCTGAAATATGAGAAG	311	
Db	173	GTTCCTTGGTTGGGGCTGGAACATTTTCTGTTGTGTGAOCTCTCTCGAATTAATGAGAAG	232	
QY	312	GCGACAAATACTACTACACAGAAAAATCCTTGGGTCAACATTGGCCGTGCCCCAGGG	371	
Db	233	TCTGACAGTACTATTATACAGAGAAATTTCTCGAACTGCCCTTGGCCCTGGCAGACA	292	
QY	372	TCGTGCTCTCTGCTTGAATTTTAAACAGCACGCTGATCCTGCTCTCTGTGTGTCGAATCTG	431	
Db	293	TCTGCTTTGTGCGCTGAATTTTAAACAGCATGGTGATCCTGATTCCTGTGTGTCGAAATCTG	352	
QY	432	CTGTGCTTCTCTGAGGGCACCTGCTCATTTTGCAGCGGCACACTGAGAAAGCAATTTGGAT	491	
Db	353	CTCTCTCTCTCTGAGGGCACCTGCTCATTTTGCACCAACACGCTGAGAAAGCAATTTGGAT	412	
QY	492	CACAACCTCACTTTCACAAGCTGGTGGCCATATATGATCTGCCCTACATACAGCTATTCAAC	551	

D	b	413	CACAACTCCACTTCCATAAGCTGGTGCAATATGATCTGCATATTACAGCTATTTCAT	472
Q	y	552	ATCATTTGACACACTGTTTAACTTTGACTGCTATAGCAGAAGCCGACAGGCCACAGATGGC	611
D	b	473	ATCATTTGACACATCTATTTTAACTTTGAACCGCTACGATGAAGCCAAACAGGCCATGATGGA	532
Q	y	612	TCCCTTGGCTCCATTCTCTCCAGCCATCTCATGATGAGAAAAAGGGGGGTTCTTGGCTA	671
D	b	533	TCTCTTGGCTCTGTGTCTCTCCAGCCATTCCATCCGGAGAAA--GAAGATTCTTTGGCTA	589
Q	y	672	AATCCCATCCAGTCCCGAAACAACGACAGTGGAGTAGTGACATTCACACAGCGTTTCTCGT	731
D	b	590	AATCCCATCCAGTCTCCAAACGTCACAGTGTATGTCAGCATTTACCAGTATTGCTGCG	649
Q	y	732	CTCACTGGAGTGATCATGACAAATAGCCCTTGATTTCTCATGTGTAACTTTAGCTACTGAGTTC	791
D	b	650	CTTACTGGAGTGGTCGCCACTGTGGCTTTGGTTCTCATGTGTAACTTCAGCTATGGAGTTT	709
Q	y	792	ATCCGAGGAGTTATTTTGAAGTCTTCTGGTATATCTCACCACTTTTTTATCTTCTATATC	851
D	b	710	ATCCGAGGAATTATTTTGAAGTCTTCTGGTATACACATCACCTTTTCATCATCTATATC	769
Q	y	852	CTTGGCTTAGGATTCACGGCATTTGGTGGAAATGTTCGGGGTCAAACAGAGGAGAGCATG	911
D	b	770	ATCTGCTTAGGGATCCATGGCTCGGGGGATGTTCGGGGTCAAACAGAAAGAGAGCATG	829
Q	y	912	AATGAGAGTCATCTCGCAAGTGTGCAGAGTCTTTTGAGATGTGGAGTATCGTGACTCC	971
D	b	830	AGTGNAAGTCATCCCGCACTGTTTCATCTTTTCCAGAGTGGGATTAAGTATGAAGG	889
Q	y	972	CACGTAGCGGCCCTTAAGTTTGAAGGGCATCCCCCTCAGTCTTGGAAGTGGATCCTTGCA	1031
D	b	890	AGTTGCAGGAGTCTCTATTTTGTGGGGCAACCCCCTGAGTCTTGGAAGTGGATCCTCGG	949
Q	y	1032	CGGTCATTCTTTATATCTGTGAAGATCCTCCGGTTTTTACCGCTCCAGCAGAGGTT	1091
D	b	950	CCGATTCGCTTTTATATCTTTGAAGAGATCCTTCGCTTTTATCGCTCCCGCAGAAGTC	1009
Q	y	1092	GTGATTACCAAGTGTGTATGCACCCCATCAAAGTTTTTGAATTCAGATGCAACAAGCT	1151
D	b	1010	GTGATTACCAAGTGTGTATGCACCCCATGTAAAGTTTTTGAATTCAGATGAGAAGCGG	1069
Q	y	1152	GGCTTCAGCATGGAAGTGGGCACTATCTTTGTTAAATTCGCCCTCAATCTCTCTCCTG	1211
D	b	1070	GGCTTTACTATGGAATAGGACAGTATATATTCGTAATTCGCCCTCGATTTCTCTCTG	1129
Q	y	1212	GAATGGCATCCTTTTACTTTTGACCTCTGCCAGAGGAAGATTTCTTCCATTCATATC	1271
D	b	1130	GAATGGCATCCTTTTACTCTGACCTCTGCTCCAGAGGAAGATTTTCTCCATTCATATT	1189
Q	y	1272	CGACACAGGGGACTGGACAGAAAATCTCATAGGGCTTTTGAACAAACAATATTCACCA	1331
D	b	1190	CGACACAGGGGACTGGACAGAAAATCTCATAGGACATTTGAACAACAGCACTCACCA	1249
Q	y	1332	ATTTCCAGGATTGAAGTGGATGTGTCCTTTGGCACACGCACTGAGGATGTTTCCAGTAT	1391
D	b	1350	ATGCCACAGGATCGAGGTGGATGTGTCCCTTTGGCACACGTCAGTGGAGATGTTCTCCAGTAC	1309
Q	y	1392	GAACTGGCTGTGCTGGTTGGAGCAGGAATTTGGGTCAACCCCTTTGCTTCTATCTGAAA	1451
D	b	1310	GAACTGGCTGTACTGGTTGGGGCAGGAATTTGGGTCACTCCCTTTGCTTCTCTTTGAAA	1369
Q	y	1452	TCCATCTGGTACAAATTCAGTGTGCAGACCAACAACCTCAAAAACAAAAAGATCTATTTTC	1511
D	b	1370	TCTATCTGGTACAAATTCACAGCGTGCACACAAAGCTGAAAAACAAAAAGATCTATTTTC	1429
Q	y	1512	TACTGGATCTGCAGGNAGACAGGTGCTTTTCTGGTTCAACAACTGTTGACTTCCCTG	1571
D	b	1430	TACTGGAAATTTGTAGAGAGACGGGTGCTTTTGGCTGGTTCAACAACATTTATGAATTTCCCTG	1489
Q	y	1572	GAAACAGGAGATGGAGGAATTTAGGCAAGTGGGTTTTTCTAAACTACCGTCTCTTCTCTCAAC	1631

Db 1747 GGTTCCTTAAGCGCCCTCCGACTTTGGCAAAAGGCTGGCAATGCTGTCGGCGTA 1806
Qy 1847 TTCAGTCTGATCTAGAAAGTTCAATCTACTTCAACAAAGAAATTTTCAGTTAT 1906
Db 1807 CTCAGTCTGATCTAGAAAGTTCAATCTACTTCAACAAAGAAAGTTTCTGAATTGG 1866
Qy 1907 AGGAATAGGACGGTAAT 1924
Db 1867 AGGAAGCGCACAGTAGT 1884

RESULT 4

US-09-023-655-1379
; Sequence 1379, Application US/09023655
; Patent No. 6607879
; GENERAL INFORMATION:
; APPLICANT: Cocks, Benjamin G.
; APPLICANT: Susan G. Stuart
; APPLICANT: Jeffrey J. Seilhamer
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE
; TITLE OF INVENTION: EXPRESSION
; NUMBER OF SEQUENCES: 1508
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION NUMBER: US/09/023,655
; FILING DATE: HEREWITH
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Zeller, Karen J.
; REGISTRATION NUMBER: 37,071
; REFERENCE/DOCKET NUMBER: PA-0001 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 855-0555
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 1379:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4267 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GENBANK
; CLONE: g37983
; US-09-023-655-1379

Query Match 22.2%; Score 579.4; DB 4; Length 4267;
Best Local Similarity 60.0%; Pred. No. 7.6e-140;
Matches 1033; Conservative 0; Mismatches 666; Indels 24; Gaps 3;

Qy 205 CAATGGAAACTGGGTGTTAAACCACTGGTTTTCAGTTTGTCTGTTGTTGTTAG 264
Db 14 CATCGGGAACTGGGCTGTGAATAGGGGCTCTCCATTTTTCATTCTGTTTGGCTGG 73
Qy 265 GCGTGAATGTTTCTGTTTGGATGCTTCTGAAATATGAGAGGCCGCAAAATAC 324
Db 74 GGTGAAACGCTCTTCTCTTTGTTGTTATACCGGGTTTATGATATTCACCTAAGTTCT 133

Qy 325 ACTACACAAGAAATCCTTTGGGTCAACATTTGGCCTGTGCCGAGCGCTCTGCTCTGCT 384
Db 134 TTTACACAAGAAATCCTTTGGGTCAACATTTGGCCTGTGCCGAGCGCTCTGACCTGCC 193
Qy 385 TGAATTTTACACAGCCTGATCTCTGCTTCTGCTGTGCTGCGAATCTGCTTCCTTCGA 444
Db 194 TGAATTTTCAACTGCATGCTGATTTCTTTGTCAGTCTGTGAAATCTGCTGCTTCCTCA 253
Qy 445 GGGGACCTGCTCATTTTTCAGCGCCACACATGTAGAAAGCAATGTGATCACAACCTCACCT 504
Db 254 GGGGTTCCAGTGGCTGCTCAACAGAGTTTGAAGACAACTGGACAGAATCTCACCT 313
Qy 505 TCCACAAGCTGGTGGCTATATGATCTGCTACATACAGCTATTTCAATTTTGTCTGAAAGAA 564
Db 314 TCCATAAAATGGTGGCATGGATGATTGCACCTTCACTCTGCGATTACACCATTTGCACATC 373
Qy 565 TGTTTAACTTTGACTGCTATAGCAGAAAGCCGACAGGCCACAGATGGCTCCCTTGCCTCCA 624
Db 374 TATTTAATGTGGAATGGTGTGTAATGCCCGAGTCAATTAATCTGATCTCTTATTCAGTAG 433
Qy 625 TTCTCTCCAGCCTATCTCATGATGAGAAAGGGGGTTCCTGGCTAAATCCCACCTCAGT 684
Db 434 CACTCTCTGNACTTGGAGACAGCAAAATGAAAGTTTATCTCAATTTTGTCTGAAAGAA 493
Qy 685 CCGAAACACGACAGTGG--AGTATGTGACATTTCCACGAGCTTGTGCTCTCACTGGAG 741
Db 494 TAAAGAACCTGAAAGGAGGCTGTACCTGGCTGTGACCTGTTGGCAGGCACTCACTGGAG 553
Qy 742 TGATCATGACATAGCCTTGAATCTCATGTTAACTTCAATTTTCTCTATATCTCTGGCTTAG 801
Db 554 TTGTCATCAGCTGTGCTCATATTAATTAATTTCTCTCCACCAAAACCATCCGAGGT 613
Qy 802 GTTATTTTGAAGTCTTCTGCTATCTACACACCTTTTATCTCTATATCTCTTGGCTTAG 861
Db 614 CTTACTTTGAAGTCTTTTGGTACACACATCACTCTTTGTGATCTTCTTCAATTTGGCTTG 673
Qy 862 GGAATCACGGCATTTGGTGAATTTGTCGGGGTCAACACAGAGGAGCATGAATGAGATC 921
Db 674 CCATCCATGGAGCTGAACGAATTTGTACGTGGGCGAGCCGACAGAGTTTGGCTGTGCATA 733
Qy 922 ATCCTCGCAAGTGTGCAGAGTCTTTTGAGATGTGGGATGATGTGATCTCCCATGTAGGC 981
Db 734 ATATAACAGTTTGTGAACAAAAAATCTCAGAATGGGGAAAAATAAA--GGAATGCCCAA 790
Qy 982 GCCCTAAGTTTGAAGGGCATCCCTCTGAGTCTTGAAGTGGATCTTGCACCGGTCAATC 1041
Db 791 TCCCTCAGTTTGTGAAACCTCTCTATGACTTGGAAATGGATAGTGGGTCCCATGTTTC 850
Qy 1042 TTTATATCTGTGAAGAGATCTCCGGTTTTCACGCTCCACAGAGAGGTTGTGATTACCA 1101
Db 851 TGTATCTCTGTGAGAGGTTGTGCGGTTTGGCGATCTCAACAGAAGTGGTTCATCACC 910
Qy 1102 AGGTTGTTATGACCCATCCAAAGTTTGGAAATTCAGATGCAAGAGCTGGCTTCCAGCA 1161
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Db 971 TGGAAAGTGGGCAATACATTTTGTCAAGTGGCCCAAGGTGTCAGAGCTGGAGTGGCAC 1030
Qy 1222 CTTTACTTTTGTGACCTTGTCTCCAGAGGAGATTTCTTCTTCCATTCATATCCAGAGCAG 1281
Db 1031 CTTTTCATCTGACATCCGCCCCCTGAGGAAGACTCTTTAGTATATCCATATCCGCATCGTTG 1090
Qy 1282 GGGACTGACAGAAATCTCATAGGGCTTTCG-----AACAACT 1323
Db 1091 GGGACTGACAGAGAGGGCTGTTTCAATGCTGTGGCTGTGTAAGCAGGAGTTTCAAGATG 1150
Qy 1324 ATTCAACAAATCCCAGGATGAAAGTGGATGGTCCCTTTGGCACAGCCAGTGGAGTATTT 1383
Db 1151 CGTGGAAACTACCTAAGATAGCGGTTGATGGCCCTTTGGCAGCTGCCAGTGAAGATGT 1210
Qy 1384 TCCAGTATGAAGTGTGCTGTGGTTGGAGCAGGAATTTGGGGTTCACCCCTTTTGTCTTA 1443

Db 1211 TCAGCTATGAGTGGTGTATGTTAGTGGAGCAGGATTTGGGTCACACCTTTCGCATCCA 1270
 QY 1444 TCTTGAATCCATCTGCTACAAATTCAGTGTGAGACCAACAACTCAAAACAAAAAGA 1503
 Db 1271 TTCTCAAGTCAGTCTGTTACAAATTTGCAATACAGCCACCAATCTGAAGCTCAAAAGA 1330
 QY 1504 TCTATTCTACTGATCTGAGGAGACAGGTGCTTTTCTGTTTCAACAACTGTGTGA 1563
 Db 1331 TCTACTTCTACTGCTGTGCGGACACACATGCTTTTGAAGTGTGTCAGATCTGCTGC 1390
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 Db 1391 AACTGCTGGAGAGCAGATGAGGAAGAACTATGCGGCTTCTCAGCTACAACTCT 1450
 QY 1624 TCTTCACCGGATGGACAGCAATATTTGTTGTCATGACGATTAACCTTTGACAAGGCCA 1683
 Db 1451 ACCTCACTGGCTGGATGAGTCTCAGGCCAATCACTTTGCTGTGCACCATGATGAGGAGA 1510
 QY 1684 CTGACATCTGACAGTCTGAAACAGAAACCTCTTTGGGAGACCAATGTGGACAAATG 1743
 Db 1511 AAGATGTGATCACAGGCTGAAACAAAGACTTTTGTATGGACGGCCCAACTGGGATAATG 1570
 QY 1744 AGTTTCTACAAATGACTACCTCCACCCCAAGTCTGTAGTGGAGTCTTCTTATGTGCC 1803
 Db 1571 AATTCAAGACAATTGCAAGTCAACACCTTAATACCAAGATAGGAGTTTCTCTGTGGAC 1630
 QY 1804 CTCGGACTTTGGCAAGAGCCTGGCCAAATGCTGTCAACGATATTCAGTCTGGATCCTA 1863
 Db 1631 CTGAAGCTTGGCTGAAACCTGAGTAAACAAAGCATCTCCAACTCTGAGTCTGGCCCTC 1690
 QY 1864 GAAAGTTCAATTTACTTCAACAAAGAAATTTTGTGATAT 1906
 Db 1691 GGGAGTGATTTTATTTTCAACAAAGAAACTTCTAACTGTG 1733

RESULT 5

US-09-437-568A-3
 ; Sequence 3, Application US/09437568A
 ; Patent No. 6620603
 ; GENERAL INFORMATION:
 ; APPLICANT: Lambeth, J. David
 ; APPLICANT: Griending, Kathy
 ; APPLICANT: Lassegue, Bernard
 ; APPLICANT: Arnold, Rebecca S.
 ; APPLICANT: Cheng, Guangjie
 ; TITLE OF INVENTION: No. 6620603el Mitogenic Regulators
 ; FILE REFERENCE: 05501-0103
 ; CURRENT APPLICATION NUMBER: US/09/437, 568A
 ; CURRENT FILING DATE: 1999-11-10
 ; NUMBER OF SEQ ID NOS: 61
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 3
 ; LENGTH: 2044
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (104)..(1810)
 US-09-437-568A-3

Query Match 20.0%; Score 521.2; DB 4; Length 2044;
 Best Local Similarity 57.4%; Pred. No. 6e-125;
 Matches 1012; Conservative 0; Mismatches 723; Indels 27; Gaps 3;
 QY 202 TGACAATGGGAACTGGGTGGTTAAACCACTGGTTTTCAGTTTGTGTTTGTGTTGTTGT 261
 Db 102 TCATGATGGGTGCTGGAATTTGAATGAGGGTCTCTCCACCATAATTAGTACTCTCATGGC 161
 QY 262 TAGGCTGAATGTTTCTGTTTGTGGATGCTTCTGAAATATGAAAGGCCGACAAAT 321
 Db 162 TGGGAATAAATTTTATCTGTTTATTTGACACGTTCTACTGGTATGAAGAGGAGTCTT 221

QY 322 ACTACTACAAAGAAATCCTTTGGGTCAACATTTGGCCTGTGCGGAGCGTCTGCTCTCT 381
 Db 222 TCCATTTACACAGAGTTATTTGGGTTCAACACTGGCTTGGCAGGAGCATTCGCATGT 281
 QY 382 GCTTGAATTTTAAACAGCAGCTGATCCTGCTTCTGTTGTGCGCAATCTGCTGTCCTTC 441
 Db 282 GCCTGATTTTAACTGCATCTAATTTCTAATACCTGTGAGTGAACCTTATTTCATTTCA 341
 QY 442 TGAGGGGCACTGCTCAATTTTGGAGCGGACACTGAGAAAGCAATTTGGATCAACACCTCA 501
 Db 342 TAAGAGAAACAAGTATTTTGTGTCAGAGGAGCCGTGGAGGAGCAATTAGACAAACACCTCA 401
 QY 502 CCTTCCAAAGCTGGTGGCTTATATGATCTGCCTACATACAGCTATTTCACATATTGCAC 561
 Db 402 GATTTCAAACCTGGTGGCTTATGGGATAGCTGTTAATGCAACATTCATCTGTGGCGC 461
 QY 562 ACCTGTTTAACTTTGACTGCTTATAGCAGAAAGCCGACAGGCCACAGATGGCTTCCCTTGC 621
 Db 462 ATTTCTTCAACCCTGGAAACGCTACCACTGGAGCCAGTCCGAGGAGCCGAGGACTTCTGG 521
 QY 622 CCATTTCTCGAGCTATCTCATGATGAGAAAGGGGGTCTTGGCTAATCCCATCC 681
 Db 522 CCGCACTTTCCAGCTGGGCAACACCCCTAACGAGAG-----CTACCTCAACCTGTGCC 575
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 Db 576 GGACCTTCCCAACAAACACACCACTGAATTGCTAAGCAATAGCAGGCGTCCACCGTCC 635
 QY 742 TGATCATGACAAATAGCCCTTGATTTCTCATGGTAACTTCAAGTCTAGGTTCAATCCGGAGA 801
 Db 636 TGGTGAATCTCTCTGGCTTTAGTCTTGATCATGACCTCGTCACTGAGTTTCATCAGACAGG 695
 QY 802 GTTATTTTGAAGTCTCTGCTGATFACCTCACCACTTTTATCTTCTATATCTTGGCTTAG 861
 Db 696 CTTCTATGAGTGTGTTCTGCTGACACACCACTGTTTCTGTTTCTCTTCTCTGAGCTGG 755
 QY 862 GGATTCAGGCAATTTGGTGGAAATTTGTCGGGGTCAACAGAGAGAGCATGAATGAGATC 921
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 QY 922 ATCTTCGCAAGTGTGACAGAGTCTTTTGAGATGTGGGATGATCGTGACTCCCACTGTAGGC 981
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 QY 982 GCCCTAAGTTTGAAGGCGATCCCTGAGTCTCGAAGTGGATCCTTGCACCGGTCTTC 1041
 Db 873 TGCCTCAATTTCTGGCAAGGAACCTCGGTTTGGAAATGGATTTTAGGCCCTTGGTCT 932
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 QY 1102 AGGTGTTTATGACCCATFCCAAAGTTTGGAAATTTGCAATGAGAAACAAGGCTGCTTACGA 1161
 Db 993 AGGTGGTAAAGCCACCCCTCTGGAGTCTCTGGAATCTCATGAAAGAGCGTGGCTTAAAA 1052
 QY 1162 TGGAGTGGGGTGTATATCTTGTAAATCCCTCAATCTCTCTCGAATGGCATC 1221
 Db 1053 TGGCGCCAGGCGAGTACATCTTGGTGCAGTCCGACGCAATATCTTCGCTGGAGTGGCACC 1112
 QY 1222 CTTTATCTTGAACCTCTGCTCCAGAGGAAGATTTCTTCTCCATTCATATCCGAGCAGAG 1281
 Db 1113 CTTTCACTTACCTCTGCCCCCAGGAAGACTTTTTCAGCGTGCACATCCGGGAGCAG 1172
 QY 1282 GGGACTGACAGAAATCTCATAGGGGCTTT-----CGNACAACAT 1323
 Db 1173 GAGACTGACACAGCGCTACTTGGAGGCTTTTGGGGCAGAGGAGCAGGCGCTTCCAGGAGC 1232
 QY 1324 ATTCACCAATTTCCAGGATTTGAAGTGGATGGTCCCTTTTGGCAGCAGCCAGTGAAGTGT 1383
 Db 1233 CTTGAGGCTGCAAGGCTGGCAGTGGAGCGGCTTTTGGAACTGCGCTGACAGATGAT 1292
 QY 1384 TCCAGTATGAATGGCTGTGCTGGTGGAGCAGGAATTTGGGGTCAACCCCTTTGCTTCTA 1443

Db 1293 TTCACTACCCAGTGTGTGTGCGTTCGCGGGGATCGAGTCACTCCCTTCGTGCTC 1352
Qy 1444 TCCTGAATCCATCTGGTACAAATTCAGTGTGCAGACCAACCTCAAAACAAAAAGA 1503
Db 1353 TTCTGAAATCTATATGTTACAAATGCGAGTGGGACAGACCCCACTGAAGCTGAGCAAG 1412
Qy 1504 TCTATTTCTACTGATCTGAGGAGAGACAGGTGCTTTCTCTGTTCAACACCTGTGA 1563
Db 1413 TGATTTCTACTGATTTGCGGATGCAAGAGCTTTTGTGTTGCTGATCTCTTAC 1472
Qy 1564 CTTCCTGGAACAGAGATGAGGAAATTAGGCAAGTGGGTTTCTAACTACCGTCTCT 1623
Db 1473 TCTCCTCGAAACACCGGATGAGTGAGCAGGGGAAACTCACTTCTGAGTTATCATAT 1532
Qy 1624 TCCTCAGCGATGGACAGCAATATTGTGTGATGAGCAATTAACCTTTGACAGGCCA 1683
Db 1533 TTCTTACCGGCTGGATGAAATCAGGCTCTTCACATAGCTTTACACTGGGACGAAATA 1592
Qy 1684 CTGACATCGTGACAGGTCTGAAACAGAAACCTCTTTGGGAGACCAATGTGGACAATG 1743
Db 1593 CTGACGTGATAGAGGCTTAAGCAGAGACCTTCTATGGGAGGCCCAACTGGACCAATG 1652
Qy 1744 AGTTTCTCAATAGTACCTCCACCCCAAGTCTGTAGTGGAGTCTTCTTATGTGCCC 1803
Db 1653 AGTTCAAGCAGATTCCTCAATCACTCACCAGCAGCATTTGGGTGTTCTTCTGTGGAC 1712
Qy 1804 CTGGGCTTTGGCAAGAGCCTGGGCAATGTGTGACCGATATCCAGTCTGGATCCTA 1863
Db 1713 CTAAAGCTCTCTGAGGACACTTCAAAAGATGTGCCACTTGTATTCATCAGCTGACCCCA 1772
Qy 1864 GAAAGGTTCAATTTCTACTTCAACAAAGAAATTTTGGATATAGNATAGGACGGTAA 1923
Db 1773 GAGGTGTTCAATTTCTATTACAAAGAGAGAGCTTCTAGACTTTGGAGGTCAAGTCCAGGC 1832
Qy 1924 TCTGCATTTGCTCTTTGAT 1945
Db 1833 ATTGTGTTTCAATCAAGTTAT 1854

RESULT 6
US-09-023-655-292
; Sequence 292, Application US/09023655
; Patent No. 6607879
; GENERAL INFORMATION:
; APPLICANT: Cocks, Benjamin G.
; APPLICANT: Susan G. Stuart
; APPLICANT: Jeffrey J. Seilhamer
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE
; TITLE OF INVENTION: EXPRESSION
; NUMBER OF SEQUENCES: 1508
; CORRESPONDENCE ADDRESS:
; ADDRESS: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: 508
; FILING DATE: HEREWITH
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Zeller, Karen J.

; REGISTRATION NUMBER: 37,071
; REFERENCE/DOCKET NUMBER: PA-0001 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 855-0555
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 292:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 206 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: COLNUT03
; CLONE: 1341948
US-09-023-655-292

Query Match 7.9%; Score 206; DB 4; Length 206;
Best Local Similarity 100.0%; Pred. No. 6.9e-44;
Matches 206; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 881 AATTGTCCGGGTCAACACAGAGAGCATGAATGAGAGTCATCTCGCAAGTGTGAGA 940
Db 1 AATTGTCCGGGTCAACACAGAGAGCATGAATGAGAGTCATCTCGCAAGTGTGAGA 60
Qy 941 GTCTTTGAGATGTGGATGATCGTGAATCCCACTGTAGCGCCCTAAGTTTGAAGGCA 1000
Db 61 GTCTTTGAGATGTGGATGATCGTGAATCCCACTGTAGCGCCCTAAGTTTGAAGGCA 120
Qy 1001 TCCCTCTGAGTCTTGAAGTGGATCCTTGCACCGGTCAATTTTATATCTGTGAAAGAT 1060
Db 121 TCCCTCTGAGTCTTGAAGTGGATCCTTGCACCGGTCAATTTTATATCTGTGAAAGAT 180
Qy 1061 CTCTCCGGTTTACCGCTCCCGCAGCA 1086
Db 181 CTCTCCGGTTTACCGCTCCCGCAGCA 206

RESULT 7
US-09-437-568A-47
; Sequence 47, Application US/09437568A
; Patent No. 6620603
; GENERAL INFORMATION:
; APPLICANT: Lambeth, J. David
; APPLICANT: Griendling, Kathy
; APPLICANT: Lassegue, Bernard
; APPLICANT: Arnold, Rebecca S.
; APPLICANT: Cheng, Guangjie
; TITLE OF INVENTION: No. 6620603el Mitogenic Regulators
; FILE REFERENCE: 05501-0103
; CURRENT APPLICATION NUMBER: US/09/437,568A
; CURRENT FILING DATE: 1999-11-10
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 47
; LENGTH: 3453
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (438)..(3134)
US-09-437-568A-47

Query Match 2.6%; Score 66.8; DB 4; Length 3453;
Best Local Similarity 49.0%; Pred. No. 2.9e-07;
Matches 247; Conservative 0; Mismatches 242; Indels 15; Gaps 2;
Qy 1024 TCCTGACCGGTCACTTTTATATCTGTGAAAGATCCTCCGGTTTACCGCTCCCGC 1083
Db 2239 TCCTGGTCCGGCAATCATCTATGGAGTGACAAGCTGCTGAGCTGAGCCGGAAGAGG 2298
Qy 1084 AGAAGTTGTGATTACCAAGTGTGTTATGCAACCATCAAAAGTTTGGAAATGAGATGA 1143
Db 2299 TGGAGATCAGCGTGTGAAGCGGAGCTGTGCTCCCTCAGGAGTGACCTACCTGCAATTCC 2358

4092	TG	GGG	GAC	CA	CCG	AGT	AC	CA	CC	CT	T	CA	CA	CT	CT	TG	CG	CC	CA	TG	AG	G	A	C	A	C	G	C	T	T	A	4151	
1261	CA	ATT	CA	TA	T	C	C	3	AG	C	AG	C	AG	G	G	A	C	T	G	A	C	A	A	A	A	A	A	A	A	A	A	1320	
4152	G	CT	G	C	A	T	C	3	G	G	C	A	G	C	G	G	C	C	T	G	A	C	C	A	C	T	C	G	C	T	A	4211	
1321	A	-----	A	T	T	C	A	C	A	T	T	C	C	C	A	G	A	T	T	G	A	G	T	G	A	T	G	T	G	C	C	T	1368
4212	CG	A	CG	G	G	T	G	A	C	A	3	A	T	G	T	G	C	C	A	T	A	C	C	C	A	A	A	A	A	A	A	4271	
1369	CA	G	T	C	A	G	A	G	T	G	T	T	C	C	A	G	T	A	G	A	G	T	G	C	T	G	T	G	T	G	C	A	1428
4272	G	C	A	C	A	C	A	G	A	G	T	G	C	A	T	A	G	T	T	G	A	G	T	T	G	A	G	T	T	G	A	G	4331
1429	C	C	C	C	T	T	G	C	T	C	T	A	T	C	T	T	G	A	A	A	T	C	C	A	T	C	T	G	T	A	C	A	1467
4332	C	C	C	T	T	T	G	C	T	C	A	T	C	T	C	A	A	G	C	T	G	T	C	T	T	C	A	A	G	T	C	A	4370

```

RESULT 9
US-10-204-708-10/c
; Sequence 10, Application US/10204708
; Patent No. 6677731
; GENERAL INFORMATION:
; APPLICANT: OLEK, Alexander
; APPLICANT: PIEPENBROCK, Christian
; APPLICANT: BERLIN, Kurt
; TITLE OF INVENTION: Diagnosis of Diseases Associated with DNA Replication
; TITLE OF INVENTION: by Assessing DNA Methylation
; FILE REFERENCE: 5013.1012
; CURRENT APPLICATION NUMBER: US/10/204,708
; CURRENT FILING DATE: 2003-05-06
; PRIOR APPLICATION NUMBER: PCT/EP01/03971
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: DE 10019058.8
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: DE 10032529.7
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: DE 10043826.1
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 98
; SEQ ID NO 10
; LENGTH: 6070
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-204-708-10

```

Query Match	2.1%;	Score 55.6;	DB 4;	Length 6070;
Best Local Similarity	53.2;	Pred. No. 0.0003;		
Matches 118;	Conservative 0;	Mismatches 104;	Indels 0;	Gaps 0;
QY 2388	AAAAATTTATTGAAATAATTATGATAAAAAACATAATAATAAACATPAATAATAACAAAAAT	2447		
Db 1906	ACAAACAAATTTCTATTTTAAATAATAAAAAAATCTCAAAATAATAATAATAATAAT	1847		
QY 2448	TACCGAGAACCCATCCCATATATAACACGCAACAGTGTCACATGTTTACTGTCACCTTTTGAT	2507		
Db 1846	TTCAACAACATATAAATATATCTTAAATACCAATAAACTATACACTTAAAAAATAATAATTT	1787		
QY 2508	ATGGTTTATCCAGTGTGAACAGCAATTTATTTATTTTTCCTCATCCAAAAAATAAAGGATTT	2567		
Db 1786	TATATTAATAAATTTTATCATCACACACAAAAAATAAAAAACGAAAAAATAAAAAA	1722		
QY 2568	TTTTTCATCTGAAAAAATAAAAAAATAAAAAAATAAAAAA	2609		
Db 1726	AAAAAATAAATAAAAAAATAAAAAAATAAAAAAATAAAAAA	1685		

RESULT 10

QY	1144	ACAAG---CGTGGCTTCAGCATGGGAAGTGGGGCAGTATATCTTTGTTAAATTGCCCTCAA	1200
Db	2359	AGAGGCCCCAAGGCTTTGAGTACAAGTCAGGACAGTGGGTGGGATCGCTCGCTGGGCTC	2418
QY	1201	TCCTCTCTCGTGAATGGCATCTTTTACTTTGACCTCTCTCTCCAGAGGAAGATTTCTTCT	1260
Db	2419	TGGGGACCAACCGAGTACCAACCCCTTCACACTGACCTCCGGGCCCATGAGGACACTCA	2478
QY	1261	CCATTTCATATCCGAGCAGCAGGGGACTGGACAGAAATCTCATAGGGCTTTTCGAACAAC	1320
Db	2479	GCCTGCACATCCGGGCAGTGGGGCCCTGGACCCTCGCTCAGGGAGATCTACTCATCCC	2538
QY	1321	AATA-----TTCAACCAATTCCCAGGATTCAGTGGATGGTCCCTTTGGCACAG	1368
Db	2539	CAAAGGGCAATGGCTGTGTGGTATACCCAAAGCTGTACCTTGATGACCGCTTTGGAGAG	2598
QY	1369	CCAGTCAGGAGATGTTTCCAGTATGAAGTGGCTGTGCTGGTGGAGCAGGAATTTGGGCTCA	1428
Db	2599	GCCATCAGGAGTGGCATAAATTTGAGGTGTCACTGTTGGTGGAGGGGCATTTGGGGTCA	2658
QY	1429	CCCCCTTTGCTTCTATCTTGAAATCCATCTGGTACAAATTCAGTGTGCAGACCAACAAC	1488
Db	2659	CCCCCTTTGCTTCATCCTCAAAGACCTGGTCTTCAAGTCATCCTTTGGGCAGCAAAATGC	2718
QY	1489	TCAAAACAAAAGATCTATTTCT	1512
Db	2719	TGTGTAGAAGATCTACTTCATCT	2742
RESULT 8			
US-09-437-568A-45			
; Sequence 45, Application US/09437568A			
; Patent No. 6620603			
; GENERAL INFORMATION:			
; APPLICANT: Lambeth, J. David			
; APPLICANT: Griendling, Kathy			
; APPLICANT: Lassegue, Bernard			
; APPLICANT: Arnold, Rebecca S.			
; APPLICANT: Cheng, Guangjie			
; TITLE OF INVENTION: No. 6620603el Mitogenic Regulators			
; FILE REFERENCE: 05501-0103			
; CURRENT APPLICATION NUMBER: US/09/437,568A			
; CURRENT FILING DATE: 1999-11-10			
; NUMBER OF SEQ ID NOS: 61			
; SOFTWARE: PatentIn Ver. 2.0			
; SEQ ID NO 45			
; LENGTH: 5494			
; TYPE: DNA			
; ORGANISM: Homo sapiens			
; FEATURE:			
; NAME/KEY: CDS			
; LOCATION: (155).. (4810)			
US-09-437-568A-45			

	Query Match	2.5%;	Score 65;	DB 4;	Length 5494;
	Best Local Similarity	49.9%;	Prod. NO. 1.1e-06;		
	Matches 229;	Conservative	0;	Mismatches 215;	Indels 15; Gaps 2;
QY	1024	TCCTTGCA	CCGGTCA	TCTTTATATCTGTGAAAGGATCCTCCGGTTTTACCGCTCCCGC	1083
DB	3912	TCCTGGTCC	AGCATCATCTATGGGGCGCAAGCTGGTGAGCTGAGCCGGAAGAAGG	3971	
QY	1084	AGAGGTGTG	ATACCAAGGTTGTATGCACCCCATCAAGTTTGGAAATTCAGATGA	1143	
DB	3972	TGGAGATCAG	CGTGTGTGAAGCGGAGCTGCTGCCCTCAGGAGTGACCCACTCGGGTCC	4031	
QY	1144	ACAAG- -	-CGTGGCTTCAGCATGGAAGTGGGCGAGTATATCTTTGTTAAATTCGCCCTCAA	1200	
DB	4032	AGCGGCCCC	CAGGGCTTTGAGTACAAAGTCAGGCGAGTGGGTGCGGATCGCTTTGGCTGGGCTC	4091	
QY	1201	TCTCTCTCT	CGAATGGGATCCCTTTTACTTTTCACTTCCTTGCTCCAGGGAAGATTTCTTCT	1260	

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US-09-621-976-2813
; Sequence 2813, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621.976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 2813
; LENGTH: 832
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 235..399
US-09-621-976-2813

Query Match          2.1%; Score 53.8; DB 4; Length 832;
Best Local Similarity 12.8%; Pred. No. 0.00033;
Matches 46; Conservative 162; Mismatches 150; Indels 0; Gaps 0;

QY 2252 TTGTGGTGTTCANAAATATACAACTAATCCAGGTGATTTATCAATCCAGGTGTACCA 2311
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
16 WTKKWSWSYMWYKWTYKTYWRWRKXKKKAWKYKWTWYVRYAMWGYKKKAMCR 75

QY 2312 TCTCTGAGTTTGGTTGTAATCTTTGTCCCTCCACCCACACAGAGATTTTAAGTA 2371
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
76 TKTKKKKKGYMMWYWGWRWSYMWMTWTGTGYVRSWMYWRVRCWKKKYKRTTC 135

QY 2372 GGGTGACTTTTAAATAAAATTTATGAATAAATGAATAAACAATAATAAACAAT 2431
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
136 YSSKGWTKRWKKAATTTWKKTYWAAATRYWMMWMTKRWASWYCWGWGKRWST 195

QY 2432 AAATAATAACAAATTTACCGAGACCCCATCCCATATAACACACAGTGACATGTT 2491
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
196 WRKRSYASARSARCCYSCSGWAGSKYMWWRWGRWATGAGKAWRASCMRRKRYAG 255

QY 2492 TACTGTCACTTTTGATATGTTTATCCAGTGCAACAGCAATTTATTTTGTCTAIC 2551
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
256 KSKTSYKSMWCMWTRSKYCYTARWTGYCYRGGWGRGWYASKYMWKRWWCWA 315

QY 2552 AAAAAATAAGGATTTTTCCTGAAAAAATAAATAAATAAATAAATAAATAAATAA 2609
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
316 RMYRYSTGRASWWRWRYTMMKWKYAWASAAKRWAMWAWRRACAAATATAA 373

RESULT 11
US-08-487-826B-13
; Sequence 13, Application US/08487826B
; Patent No. 5993827
; GENERAL INFORMATION:
; APPLICANT: Sim, Kim L.
; APPLICANT: Chitnis, Chetan
; APPLICANT: Miller, Louis H.
; APPLICANT: Peterson, David S.
; APPLICANT: Su, Xin-zhaun
; APPLICANT: Wellens, Thomas E.
; TITLE OF INVENTION: BINDING DOMAINS FROM PLASMODIUM VIVAX
; AND PLASMODIUM FALCIPARUM ERYTHROCYTE BINDING PROTEINS
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Knobbe Martens Olson & Bear
; STREET: 620 Newport Center Drive 16th Floor
; CITY: Newport Beach
; STATE: California
; COUNTRY: US
; ZIP: 92660
; COMPUTER READABLE FORM:

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; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/487.826B
; FILING DATE: 10-SEP-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Israelsen Ned
; REGISTRATION NUMBER: 29,655
; REFERENCE/DOCKET NUMBER: NIH121.001CP1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 235-8550
; TELEFAX: (619) 235-0176
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 19124 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
; HYPOTHEetical: NO
; ANTI-SENSE: NO
; US-08-487-826B-13

Query Match          2.0%; Score 52.8; DB 2; Length 19124;
Best Local Similarity 53.7%; Pred. No. 0.0028;
Matches 132; Conservative 0; Mismatches 112; Indels 2; Gaps 1;

QY 2366 TAAGTAGGGTGACTTTTAAATAAAATTTATTTGAATAAATTAATGATAAAACATAAAT 2425
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
186 TAATCCGAGCGAAAAAATATATATATCTCATATAAAATTTATTAATACATATAT 245

QY 2426 AAACATAAATAAACAATAATACCGAGAACCCCATCCCATATACACCAACAGTGA 2485
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
246 ATAGTTTCCTATTAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 305

QY 2486 CATGT--TTACTGTCTCACTTTTGATATGGTTTATCCAGTGTGAACAGCAATTTATTT 2543
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
306 AATATAACTAATTTCTTATTTTATTTAACTTTTATTCCTTTTAAATTTCTTATCTCT 365

QY 2544 TGCTATCAAAAAATAAAGGATTTTTTTTTCACCTTGAAAAAATAAATAAATAAATAA 2603
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
366 ATGCAACAAAAAACATAAAGTAATTTCTACATATCAACAAAAAATAAATAAATAAATAA 425

QY 2604 AAAAAA 2609
Db : : : : :
426 AAAAAA 431

RESULT 12
US-08-885-469-1
; Sequence 1, Application US/08885469
; Patent No. 6280739
; GENERAL INFORMATION:
; APPLICANT: Jacobs, Kenneth
; APPLICANT: McCoy, John M.
; APPLICANT: Racie, Lisa A.
; APPLICANT: Lavallie, Edward R.
; APPLICANT: Merberg, David
; APPLICANT: Treacy, Maurice
; APPLICANT: Spaulding, Vikki
; APPLICANT: Agostino, Michael
; TITLE OF INVENTION: SECRETED PROTEINS
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute, Inc.
; STREET: 87 Cambridgepark Drive
; CITY: Cambridge
; STATE: MA
; COUNTRY: U.S.A.
; ZIP: 02140

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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA: US/08/885,469
FILING DATE:
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Sprunger, Suzanne A.
REGISTRATION NUMBER: P-41,323
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 498-8284
TELEFAX: (617) 876-5851
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 817 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
MOLECULE TYPE: cdna
US-08-885-469-1

Query Match      2.0%; Score 52.6; DB 3; Length 817;
Best Local Similarity 75.3%; Pred. No. 0.00066;
Matches 61; Conservative 3; Mismatches 17; Indels 0; Gaps 0;

QY 2529 GCAATTTATTATTTTCTCATCAAAATAAAGGATTTTTCACCTTGAAAAA 2588
Db 737 GRAATTAATGTTAGTCGMAAATAAAGTGTTCCTTTTWTWAAAAA 796

QY 2589 AAAAAA 2609
Db 797 AAAAAA 817

RESULT 13
US-09-625-918-1
Sequence 1, Application US/09625918
Patent No. 6451318
GENERAL INFORMATION:
APPLICANT: Jacobs, Kenneth
McCoy, John M.
Racie, Lisa A.
Lavallie, Edward R.
Merberg, David
Treacy, Maurice
Spaulding, Vikki
Agostino, Michael
NUMBER OF INVENTION: SECRETED PROTEINS
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSER: Genetics Institute, Inc.
STREET: 87 CambridgePark Drive
CITY: Cambridge
STATE: MA
COUNTRY: U.S.A.
ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/625,918
FILING DATE: 26-Jul-2000
CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Sprunger, Suzanne A.
REGISTRATION NUMBER: P-41,323
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 498-8284

TELEFAX: (617) 876-5851
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 817 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
MOLECULE TYPE: cdna
US-09-625-918-1

Query Match      2.0%; Score 52.6; DB 4; Length 817;
Best Local Similarity 75.3%; Pred. No. 0.00066;
Matches 61; Conservative 3; Mismatches 17; Indels 0; Gaps 0;

QY 2529 GCAATTTATTATTTTCTCATCAAAATAAAGGATTTTTCACCTTGAAAAA 2588
Db 737 GRAATTAATGTTAGTCGMAAATAAAGTGTTCCTTTTWTWAAAAA 796

QY 2589 AAAAAA 2609
Db 797 AAAAAA 817

RESULT 14
US-09-647-390-15
Sequence 15, Application US/09647390
Patent No. 6465836
GENERAL INFORMATION:
APPLICANT: Stuiver, Maarten
APPLICANT: Custers, Jerome
APPLICANT: Simons, Lambertus
TITLE OF INVENTION: Pathogen-Inducible Promoter
FILE REFERENCE: MCG 5:707/UST
CURRENT APPLICATION NUMBER: US/09/647,390
CURRENT FILING DATE: 2000-09-29
PRIOR APPLICATION NUMBER: EP 98201024.1
PRIOR FILING DATE: 1998-04-01
PRIOR APPLICATION NUMBER: PCT/EP99/02178
PRIOR FILING DATE: 1999-03-25
NUMBER OF SEQ ID NOS: 18
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 15
LENGTH: 3680
TYPE: DNA
ORGANISM: Helianthus annuus
FEATURE:
NAME/KEY: promoter
LOCATION: (1)..(1889)
NAME/KEY: CDS
LOCATION: (1890)..(3503)
US-09-647-390-15

Query Match      2.0%; Score 51.2; DB 4; Length 3680;
Best Local Similarity 52.9%; Pred. No. 0.0032;
Matches 110; Conservative 0; Mismatches 98; Indels 0; Gaps 0;

QY 2401 ATAATTAATGATAAAACATAATAATAACATAATAATAACATAATAACGAGTGTACATGTTTACTGTCTACATTTTGTGATGTTTATCCAG 2460
Db 691 ATAAATAATTTTATTAATAATAATGAAATTTTAAATAAGATCATTTTCTTAAATCC 750

QY 2461 ATCCCCATATAACACCAACAGTGTACATGTTTACTGTCTACATTTTGTGATGTTTATCCAG 2520
Db 751 GTAGCGAGTAAAGTTATGATGTTTCTAACTTTTATGTTTCTTATTTCTATCTGTTT 810

QY 2521 TGTGAACGCAATTTATTTTGTCTATCAAAATAAAGGATTTTTCACCTTGA 2580
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QY 2581 AAAAAA 2608
Db 871 AAAAAA 898
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: July 23, 2004, 08:30:25 ; Search time 1142 Seconds
(without alignments)
11167.752 Million cell updates/sec

Title: US-10-618-839-1

Perfect score: 2609

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Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 3216467 seqs, 244149694 residues

Total number of hits satisfying chosen parameters: 6432934

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2605	99.8	2609	13	US-09-878-722-244
2	2605	99.8	2609	13	US-09-878-722-244
3	2605	99.8	2609	15	US-10-157-031-174
4	2605	99.8	2609	15	US-10-318-906A-1
5	2605	99.8	2609	15	US-10-318-906A-1
6	2605	99.8	2609	15	US-10-318-906A-1
7	2605	99.8	2609	15	US-10-318-906A-1
8	2605	99.8	2609	15	US-10-318-906A-1
9	1305	50.0	2577	15	US-10-318-906A-22
10	1305	50.0	2577	15	US-10-318-906A-22
11	1182.8	45.3	2619	15	US-10-318-906A-41
12	1182.8	45.3	2619	15	US-10-318-906A-41
13	797	30.5	797	17	US-10-618-839-15
14	582	22.3	4266	13	US-10-342-887-480

15	582	22.3	4266	13	US-10-172-118-480	Sequence 480, App
16	582	22.3	4266	13	US-10-418-036-1	Sequence 1, Appli
17	582	22.3	4266	15	US-10-261-078-18	Sequence 18, Appl
18	582	22.3	4324	15	US-10-240-965-196	Sequence 196, App
19	579.4	22.2	4267	15	US-10-171-581-257	Sequence 257, App
20	579.4	22.2	4267	17	US-10-641-643-1379	Sequence 1379, App
21	551.6	21.1	658	15	US-10-157-031-175	Sequence 175, App
22	521.2	20.0	2044	9	US-09-999-248-6	Sequence 6, Appli
23	521.2	20.0	2044	13	US-10-418-036-5	Sequence 5, Appli
24	521.2	20.0	2044	15	US-10-318-906A-3	Sequence 3, Appli
25	521.2	20.0	2044	15	US-10-319-236A-3	Sequence 3, Appli
26	521.2	20.0	2044	17	US-10-618-839-3	Sequence 5, Appli
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c	511.8	19.6	531	15	US-10-066-543-3290	Sequence 3290, Ap
28	501.2	19.2	560	12	US-09-969-034-1969	Sequence 1969, Ap
30	496.8	19.0	509	15	US-10-066-543-2589	Sequence 2589, Ap
c	479.2	18.4	503	15	US-10-225-486-34	Sequence 34, Appl
32	478.6	18.3	555	9	US-09-878-178-519	Sequence 519, App
33	478.6	18.3	555	14	US-10-046-935-519	Sequence 519, App
c	468.6	18.0	491	13	US-10-146-502-519	Sequence 519, App
c	468.6	18.0	491	13	US-09-878-722-227	Sequence 227, App
c	468.6	18.0	491	13	US-09-904-456-227	Sequence 227, App
38	460.4	17.6	562	12	US-09-969-034-1885	Sequence 1885, Ap
39	460.4	17.6	570	9	US-09-878-178-1857	Sequence 1857, Ap
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ALIGNMENTS

RESULT 1

US-09-878-722-244
; Sequence 244, Application US/09878722
; Publication No. US20020040127A1
; GENERAL INFORMATION:
; APPLICANT: Jiang, Yugu
; APPLICANT: Hepler, William T.
; APPLICANT: Clapper, Jonathan
; APPLICANT: Wang, Aijun
; APPLICANT: Secrist, Heather
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF COLON CANCER
; FILE REFERENCE: 210121.524
; CURRENT APPLICATION NUMBER: US/09/878,722
; CURRENT FILING DATE: 2001-06-08
; NUMBER OF SEQ ID NOS: 245
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 244
; LENGTH: 2609
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(2609)
; OTHER INFORMATION: n = A,T,C or G
US-09-878-722-244

Query Match 99.8%; Score 2605; DB 13; Length 2609;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2609; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db

1 GCTGATAGCACAGTCTCTCTCCAGAGAGGCGGAATAAACTTATTTCATTCCTCCAGAA 60

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 Db 361 GTGCCCGAGGCTGTCTCTGTCTGCTTGAATTTTACAGCAGCCTGATCTCTGCTTCTGT 420
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 Qy 1861 CTAGAAGGTTCAATCTTACTTCAACAGAAAATTTTGGAGTTATAGGAATAAGACGG 1920
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RESULT 2

US-09-904-456-244

; Sequence 244, Application US/09904456

; Publication No. US20030017167A1

; GENERAL INFORMATION:

; APPLICANT: Jiang, Yugui

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY

; FILE OF INVENTION: AND DIAGNOSIS OF COLON CANCER

; FILE REFERENCE: 210121.324CI

; CURRENT APPLICATION NUMBER: US/09/904,456

; CURRENT FILING DATE: 2001-07-11

; NUMBER OF SEQ ID NOS: 247

; SOFTWARE: Fast-Seq for Windows Version 4.0

; SEQ ID NO 244

; LENGTH: 2609

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: misc feature

; LOCATION: 2025_2036, 2164, 2264

; OTHER INFORMATION: n = A,T,C or G

US-09-904-456-244

Query Match 99.8%; Score 2605; DB 13; Length 2609;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2609; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 181 GAAGGCTCCAAACCAACCTCTTGACAAATGGGAACTGGGTGGTTAACCACTGGTTTTCAG 240
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QY 241 TTTTGTCTGCTGTTGTTGGTTAGGCTGAATGTTTCTGTTGTTGGATGCTTCTCGA 300
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QY 241 TTTTGTCTGCTGTTGTTGGTTAGGCTGAATGTTTCTGTTGTTGGATGCTTCTCGA 300
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Db 301 AATATGAGAAGCCGACAAATACTACTACACAAGAAATCTCTGGGTCAACATTTGGCCT 360
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QY 541 CAGCTATTACATCAATTTGACACCTGTTAACTTTGACTGCTATAGCAGAAAGCGCAGG 600
Db 541 CAGCTATTACATCAATTTGACACCTGTTAACTTTGACTGCTATAGCAGAAAGCGCAGG 600
QY 601 CCACAGATGGCTCCCTTGGCTCCATTTCTCCAGCCTATCTCATGATGAGAAAAAGGGG 660
Db 601 CCACAGATGGCTCCCTTGGCTCCATTTCTCCAGCCTATCTCATGATGAGAAAAAGGGG 660
QY 661 GTTCTTTGGCTAAATCCATCCAGTCCCGAAAACAGCAGTGGAGTATGTACATTTCAACA 720
Db 661 GTTCTTTGGCTAAATCCATCCAGTCCCGAAAACAGCAGTGGAGTATGTACATTTCAACA 720
QY 721 GCGTTCTCTGTCTCACTGGAGTATCATGACAAATAGCTTGAATCTCATGTTAACTTCAG 780
Db 721 GCGTTCTCTGTCTCACTGGAGTATCATGACAAATAGCTTGAATCTCATGTTAACTTCAG 780
QY 781 CTACTCAGTTTCATCCGGAGGATTTTGAAGTCTTCTGGTATCTCAGCACCTTTTAA 840
Db 781 CTACTCAGTTTCATCCGGAGGATTTTGAAGTCTTCTGGTATCTCAGCACCTTTTAA 840
QY 841 TCTTCTATATCTCTTGGCTTAGGGAATTCACGGCAATGGTGAATTTGCCGGGTCAACAC 900
Db 841 TCTTCTATATCTCTTGGCTTAGGGAATTCACGGCAATGGTGAATTTGCCGGGTCAACAC 900
QY 901 AGGAGAGATGAATGAGAGTCACTCCGCAAGTGTGCAGAGTCTTTTGAGATGTGGGATG 960
Db 901 AGGAGAGATGAATGAGAGTCACTCCGCAAGTGTGCAGAGTCTTTTGAGATGTGGGATG 960
QY 961 ATCTGTACTCCCACTGTAGCGCCCTAAGTTTGAAGGCAATCCCTGAGTCTTGAAGT 1020
Db 961 ATCTGTACTCCCACTGTAGCGCCCTAAGTTTGAAGGCAATCCCTGAGTCTTGAAGT 1020
QY 1021 GGATCCTTGACCGGTCAATCTTTATATCTGTGAAGAGTCCCTCCGGTTTACCGCTCCC 1080
Db 1021 GGATCCTTGACCGGTCAATCTTTATATCTGTGAAGAGTCCCTCCGGTTTACCGCTCCC 1080
QY 1081 AGCAGAGTTGTGATACCAAGTTGTATGCAAGTCCCAAGTCTTGAAGTTTGAAGTTGACA 1140
Db 1081 AGCAGAGTTGTGATACCAAGTTGTATGCAAGTCCCAAGTCTTGAAGTTTGAAGTTGACA 1140
QY 1141 TGAACAAGCGTGGCTTTCAGATGGAAGTGGGCGAGTATATCTTTGTAATGCCCTCAA 1200
Db 1141 TGAACAAGCGTGGCTTTCAGATGGAAGTGGGCGAGTATATCTTTGTAATGCCCTCAA 1200
QY 1201 TCTCTCTCTGGAATGGCATCTTTTACCTTTGACCTCTGCTCCAGAGGAAGATTTCTTCT 1260
Db 1201 TCTCTCTCTGGAATGGCATCTTTTACCTTTGACCTCTGCTCCAGAGGAAGATTTCTTCT 1260
QY 1261 CCATTTCATATCCGAGCAGGAGGACTGACAGAAATCTCATAGGGCTTTGCAACAC 1320
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QY 1321 AATATTACCAATTTCCAGGATTTGAAGTGGTGGTCCCTTTGGCAGCAGCGAGTGGATG 1380
Db 1321 AATATTACCAATTTCCAGGATTTGAAGTGGTGGTCCCTTTGGCAGCAGCGAGTGGATG 1380
QY 1381 TTTTCCAGTATGAAGTGGTGTCTGTGGTGGAGGAAATTTGGGTTCACCCCTTTGCTT 1440

Db 1381 TTTTCCAGTATGAAGTGGTGTCTGTGGTGGAGCAGGAATTTGGGTTCACCCCTTTGCTT 1440
QY 1441 CTATCTTGAATCAATCTGTACAAATTTCCAGTGTGAGACCAACCACTCAAAACAAAA 1500
Db 1441 CTATCTTGAATCAATCTGTACAAATTTCCAGTGTGAGACCAACCACTCAAAACAAAA 1500
QY 1501 AGATCTATTTCTACTGATCTGCAGGGAGACAGGTGCTTTTCTGTGTTCAACAACCTGT 1560
Db 1501 AGATCTATTTCTACTGATCTGCAGGGAGACAGGTGCTTTTCTGTGTTCAACAACCTGT 1560
QY 1561 TGACTTCCCTGGAAACAGGAGATGAGGAATTAGGCAAGTGGGTTTTCTAAACTACCGTC 1620
Db 1561 TGACTTCCCTGGAAACAGGAGATGAGGAATTAGGCAAGTGGGTTTTCTAAACTACCGTC 1620
QY 1621 TCTTCTCTCACCGGATGGGACAGCAATATTTGCTCATGCAGCATTAACCTTTTGACAAGG 1680
Db 1621 TCTTCTCTCACCGGATGGGACAGCAATATTTGCTCATGCAGCATTAACCTTTTGACAAGG 1680
QY 1681 CCATGACATCTGTGACAGTCTGAAACAGAAAACTCTTTTGGGAGACCAATGTGGACA 1740
Db 1681 CCATGACATCTGTGACAGTCTGAAACAGAAAACTCTTTTGGGAGACCAATGTGGACA 1740
QY 1741 ATGAGTTTCTCAATAGCTACTCTCCACCCCAAGTCTGTAGTGGAGTTTCTTATGTG 1800
Db 1741 ATGAGTTTCTCAATAGCTACTCTCCACCCCAAGTCTGTAGTGGAGTTTCTTATGTG 1800
QY 1801 GCGCTCGGACTTTGGCAAGAGCCTGCGCAAAATGCTGTCCAGCATATTCAGTCTGGATC 1860
Db 1801 GCGCTCGGACTTTGGCAAGAGCCTGCGCAAAATGCTGTCCAGCATATTCAGTCTGGATC 1860
QY 1861 CTAGAAGGTTTCAATCTACTTTCAACAAAGAAAAATTTTGGAGTTATAGGAATAAGGACGG 1920
Db 1861 CTAGAAGGTTTCAATCTACTTTCAACAAAGAAAAATTTTGGAGTTATAGGAATAAGGACGG 1920
QY 1921 TAATCTGCAATTTGCTCTTGTATCTTCAGTAAATGAGTTATAGGAATAAGGACGGTAA 1980
Db 1921 TAATCTGCAATTTGCTCTTGTATCTTCAGTAAATGAGTTATAGGAATAAGGACGGTAA 1980
QY 1981 TCTGCAATTTGCTCTTGTATCTTCAGTAAATGAGTTATAGGAATAAGGACGGTAA 1980
Db 1981 TCTGCAATTTGCTCTTGTATCTTCAGTAAATGAGTTATAGGAATAAGGACGGTAA 1980
QY 2041 CACTTTAGGATGAAGTGTGCTCTCAAGCTTGAATCTCCTGATTTCTTTTGTGATG 2100
Db 2041 CACTTTAGGATGAAGTGTGCTCTCAAGCTTGAATCTCCTGATTTCTTTTGTGATG 2100
QY 2101 CATTCAACTTCTGATCTTGAAGTCTCAGCACTTGAAGTCTTGAAGTCTTGAAGTCT 2160
Db 2101 CATTCAACTTCTGATCTTGAAGTCTCAGCACTTGAAGTCTTGAAGTCTTGAAGTCT 2160
QY 2161 GAANTTTCTTAAAGCCCATGGATCTTCTCAGAAAAATAACTGTAATCTTTTCTGACAG 2220
Db 2161 GAANTTTCTTAAAGCCCATGGATCTTCTCAGAAAAATAACTGTAATCTTTTCTGACAG 2220
QY 2221 CCATGATGTAGCAAGGCTTGATAGCAAGTGTGGTGTCCANAATATATCAACTAATC 2280
Db 2221 CCATGATGTAGCAAGGCTTGATAGCAAGTGTGGTGTCCANAATATATCAACTAATC 2280
QY 2281 CCAGTGTATTTATCAATTTCCAGTGTACCCTCTCCTGAGTTTGGTGTGTAATCTTTG 2340
Db 2281 CCAGTGTATTTATCAATTTCCAGTGTACCCTCTCCTGAGTTTGGTGTGTAATCTTTG 2340
QY 2341 TCCCTCCCAACCCCAAGAGATTTTAAAGTGGGTGACTTTTAAATAAAAAATTTATTGA 2400
Db 2341 TCCCTCCCAACCCCAAGAGATTTTAAAGTGGGTGACTTTTAAATAAAAAATTTATTGA 2400
QY 2401 ATAATTAATGATAAACAATAATAATAATAATAATAATAATAATAATAATAATAATAATA 2460
Db 2401 ATAATTAATGATAAACAATAATAATAATAATAATAATAATAATAATAATAATAATAATA 2460
QY 2461 ATCCCATATACCAACAGTGTACATGTTTACTGTCTCATTGTGATATGTTTATCCAG 2520
Db 2461 ATCCCATATACCAACAGTGTACATGTTTACTGTCTCATTGTGATATGTTTATCCAG 2520

[illegible]

Db	2401	ATAATTAAATGATAAAACATAATAATAAAACATAAAATAAAACAAAAATTAACGAGAACCCC	2460
Qy	2461	ATCCCCATATACCAACACAGTGACATGTTTACTGTGCACATTTTGATATGTTTATCCAG	2520
Db	2461	ATCCCCATATACCAACACAGTGACATGTTTACTGTGCACATTTTGATATGTTTATCCAG	2520
Qy	2521	TGTGAACAGCAATTTATTATTTTGGCTCATCAAAAAATAAAGGATTTTTTTCACATTGAA	2580
Db	2521	TGTGAACAGCAATTTATTATTTTGGCTCATCAAAAAATAAAGGATTTTTTTCACATTGAA	2580
Qy	2581	AAAAAAAAAAAAAAAAAAAAAAAAAAAAA	2609
Db	2581	AAAAAAAAAAAAAAAAAAAAAAAAAAAAA	2609

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RESULT 5
US-10-319-236A-1
; Sequence 1. Application US/10319236A
; Publication No. US20030166198A1
; GENERAL INFORMATION:
; APPLICANT: Lambeth, J. David
; APPLICANT: Griendling, Kathy
; APPLICANT: Lassegue, Bernard
; APPLICANT: Arnold, Rebecca S.
; APPLICANT: Cheng, Guangjie
; TITLE OF INVENTION: Antibodies to Mitogenic Oxygenases
; FILE REFERENCE: 03501-0220 (43150-281176)
; CURRENT APPLICATION NUMBER: US/10/319,236A
; CURRENT FILING DATE: 2002-12-13
; PRIOR APPLICATION NUMBER: US 09/437,568
; PRIOR FILING DATE: 1999-11-10
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn ver. 2.0
; SEQ ID NO 1
; LENGTH: 2609
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (2025)
; OTHER INFORMATION: n at position 2025 = any nucleotide
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (2036)
; OTHER INFORMATION: n at position 2036 = any nucleotide
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (2164)
; OTHER INFORMATION: n at position 2164 = any nucleotide
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (2264)
; OTHER INFORMATION: n at position 2264 = any nucleotide
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (207)..(1901)
US-10-319-236A-1

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Query Match	99.8%;	Score 2605;	DB 15;	Length 2609;			
Best Local Similarity	100.0%;	Pred. No. 0;					
Matches 2609; Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;
Qy	1	GCTGATAGCACAGTTCTGTCCAGAGAAGGCGCGAATAAACTTATTTCATTTCCCGAGAA	60				
Db	1	GCTGATAGCACAGTTCTGTCCAGAGAAGGCGCGAATAAACTTATTTCATTTCCCGAGAA	60				
Qy	61	CTCTGGGGTAGTGTTGTTTTCACATCTTAAAGGCTTCAGACCCCTCGCGTGGCAA	120				
Db	61	CTCTGGGGTAGTGTTGTTTTCACATCTTAAAGGCTTCAGACCCCTCGCGTGGCAA	120				
Qy	121	ATGTTCCATTCCCTGGAAGGACCTCTCCAGAAATCCGGATTGCTGAATCTCCCGTTGGCTTA	180				
Db	121	ATGTTCCATTCCCTGGAAGGACCTCTCCAGAAATCCGGATTGCTGAATCTCCCGTTGGCTTA	180				

1261	QY	CGATTCATATCCAGCAGCAGCGGGA	CTGGACAGAAATCTCATAGGGCTTTTCGAACAAC	1320
1321	QY	AATATTACCAAAATCCCAAGTAATGAAGTGGATCCCTTTGGCACA	CAGCAGTGAGGATG	1380
1321	Db	AATATTACCAAAATCCCAAGTAATGAAGTGGATCCCTTTGGCACA	CAGCAGTGAGGATG	1380
1381	QY	TTTTTCCAGTATGAAGTGGCTGTGCTGGTTGGAGCAGGAATTTGGG	GTACCCCTTTGCTTT	1440
1381	Db	TTTTTCCAGTATGAAGTGGCTGTGCTGGTTGGAGCAGGAATTTGGG	GTACCCCTTTGCTTT	1440
1441	QY	CTATCTTGAATCCATCTCGTACAATTC	CCAGTGTGCAGACACAACTCTCAAAA	1500
1441	Db	CTATCTTGAATCCATCTCGTACAATTC	CCAGTGTGCAGACACAACTCTCAAAA	1500
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1501	Db	AGATCTATTTCTACTGATCTGCAGGGACAGAGTGCCTTTTCTCG	TGTTCAACACCTGT	1560
1561	QY	TGACTTCCCTGGAAACAGGAGATCGAGAAATTAGGCAAAAGTGG	TTTTCTTAAACTACCGTC	1620
1561	Db	TGACTTCCCTGGAAACAGGAGATCGAGAAATTAGGCAAAAGTGG	TTTTCTTAAACTACCGTC	1620
1621	QY	TCCTTCTCTCACCGGATGGGACAGCAATATTGTTGGTCA	TGCAGCATTTAAACTTTTGACAAGG	1680
1621	Db	TCCTTCTCTCACCGGATGGGACAGCAATATTGTTGGTCA	TGCAGCATTTAAACTTTTGACAAGG	1680
1681	QY	CCACTGACATCGTGACAGGTC	TGAAACAGAAACCTCTTTGGGACCACTG	1740
1681	Db	CCACTGACATCGTGACAGGTC	TGAAACAGAAACCTCTTTGGGACCACTG	1740
1741	QY	ATCAGTTTTTCTACAAATAGCTACCTCCACCCCAAGTCTGTAG	TGGGAGTTTTTCTTATGTG	1800
1741	Db	ATGAGTTTTTCTACAAATAGCTACCTCCACCCCAAGTCTGTAG	TGGGAGTTTTTCTTATGTG	1800
1801	QY	GCCTCTGGACATTTGGGCAAGAGCGCTCGGCAAAATGCTGTCT	CACCGATATTCAGTCTCGATC	1860
1801	Db	GCCTCTGGACATTTGGGCAAGAGCGCTCGGCAAAATGCTGTCT	CACCGATATTCAGTCTCGATC	1860
1861	QY	CTAGAAAGGTTCAATTCTACTCTTCAACAAGAAATTTTTCAG	TATTATAGGAATTAAGGACGG	1920
1861	Db	CTAGAAAGGTTCAATTCTACTCTTCAACAAGAAATTTTTCAG	TATTATAGGAATTAAGGACGG	1920
1921	QY	TAATCTGCATTTTGTCTCTTTTGATCTCTCAGTAATTCAGTTA	TATAGGAATTAAGGACCGGTAA	1980
1921	Db	TAATCTGCATTTTGTCTCTTTTGATCTCTCAGTAATTCAGTTA	TATAGGAATTAAGGACCGGTAA	1980
1981	QY	TCCTGCAATTTGTCTCTTTTGATCTCTCAGTAATTTTACTGTCT	CCTCCTCAGGTTTGANCAGT	2040
1981	Db	TCCTGCAATTTGTCTCTTTTGATCTCTCAGTAATTTTACTGTCT	CCTCCTCAGGTTTGANCAGT	2040
2041	QY	CACTTTAGGATTAAGAAATGTGCTCTCAAGCCTTGACTCCCTCG	TGTTATTTTGTATTG	2100
2041	Db	CACTTTAGGATTAAGAAATGTGCTCTCAAGCCTTGACTCCCTCG	TGTTATTTTGTATTG	2100
2101	QY	CATTCAACTCTGTTTACTGTAGCTTCAGCAACTTAAGAACTCT	GCAAGTCTCTTAAAGTTCT	2160
2101	Db	CATTCAACTCTGTTTACTGTAGCTTCAGCAACTTAAGAACTCT	GCAAGTCTCTTAAAGTTCT	2160
2161	QY	GAANNTCTTAAAGCCCATGGATCGTTCTCAGAAAAATAACTGT	GTAAATCTTTCTGGACAG	2220
2161	Db	GAANNTCTTAAAGCCCATGGATCGTTCTCAGAAAAATAACTGT	GTAAATCTTTCTGGACAG	2220
2221	QY	CCATGACTGTAGCAAGCCTTGATAGCAGAAAGTTTGGTGGTT	TCANAAATTAACAACCTAATC	2280
2221	Db	CCATGACTGTAGCAAGCCTTGATAGCAGAAAGTTTGGTGGTT	TCANAAATTAACAACCTAATC	2280
2281	QY	CCAGTGATTTTATCAATTCAGTGTGTACCATCTCCTGAGTTT	TGGTTTGTAACTTTTGTG	2340
2281	Db	CCAGTGATTTTATCAATTCAGTGTGTACCATCTCCTGAGTTT	TGGTTTGTAACTTTTGTG	2340
2341	QY	TCCCTCCCAACCCCAAGAGATTTTAAAGTAGGGTGACTTTT	TAAATAAAAAATTTATTTGA	2400
2341	Db	TCCCTCCCAACCCCAAGAGATTTTAAAGTAGGGTGACTTTT	TAAATAAAAAATTTATTTGA	2400

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RESULT 7
US-10-393-567-13
; Sequence 13, Application US/10393567
; Publication No. US20030194733A1
; GENERAL INFORMATION:
; APPLICANT: WANG, YIXIN
; TITLE OF INVENTION: CANCER DIAGNOSTIC PANEL
; FILE REFERENCE: CDS 269 US NP
; CURRENT APPLICATION NUMBER: US/10/393,567
; CURRENT FILING DATE: 2003-03-21
; PRIOR APPLICATION NUMBER: 60/368,667
; PRIOR FILING DATE: 2002-03-29
; NUMBER OF SEQ ID NOS: 100
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 13
; LENGTH: 2609
; TYPE: DNA
; ORGANISM: human
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (2025)..(2025)
; OTHER INFORMATION: any kind of base
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (2036)..(2036)
; OTHER INFORMATION: any kind of base
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (2164)..(2164)
; OTHER INFORMATION: any kind of base
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (2264)..(2264)
; OTHER INFORMATION: any kind of base
; US-10-393-567-13

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	Query Match	99.8%	Score 2605;	DB 15;	Length 2609;
	Best Local Similarity	100.0%;	Prod. No. 0;		
	Matches 2609;	Conservative	0;	Mismatches 0;	Indels 0; Gaps 0;
Qy	1	GCTGATAGCACAGTCTCTCCAGAGAGGAGCGGGAATAA	CTTATTATTC	TCCAGGAA	60
Db	1	GCTGATAGCACAGTCTCTCCAGAGAGGAGCGGGAATAA	CTTATTATTC	TCCAGGAA	60
Qy	61	CTCTTGGGGTAGGTGTGTGTTTTTTCACATCTTTAAAGGCTC	CACAGACCTCGCTGGTGGACAA	120	
Db	61	CTCTTGGGGTAGGTGTGTGTTTTTTCACATCTTTAAAGGCTC	CACAGACCTCGCTGGTGGACAA	120	
Qy	121	ATGTTTCATCTCTGAAGGACCTCCAGAAATCCGGATTGCTG	GAATCTTCCCTGTTGCGCTA	180	
Db	121	ATGTTTCATCTCTGAAGGACCTCTCAGAAATCCGGATTGCT	GAAATCTTCCCTGTTGCGCTA	180	
Qy	181	GAAGGGCTCCAAACCACTCTTTGACAATGGGAAACTGGGTGG	TTAAACCACTGGTTTTTCAG	240	
Db	181	GAAGGGCTCCAAACCACTCTTTGACAATGGGAAACTGGGTGG	TTAAACCACTGGTTTTTCAG	240	


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QY 1261 CCATTCATATCCGAGCAGAGGGGACTGGACAGAAAATCTCATATAGGGCTTTTGAACAAC 1320
Db 1261 CCATTCATATCCGAGCAGCAGGGGACTGGACAGAAAATCTCATATAGGGCTTTTGAACAAC 1320
QY 1321 AATATTACCAAATCCAGGATTTGAAGTGGATGGTCCCTTTGGCAGAGCCAGTGAGGATG 1380
Db 1321 AATATTACCAAATCCAGGATTTGAAGTGGATGGTCCCTTTGGCAGAGCCAGTGAGGATG 1380
QY 1381 TTTTCCAGTATGAAGTGGCTGTCTGTGTGGACAGGAAATGGGGTCAACCCCTTTGCTT 1440
Db 1381 TTTTCCAGTATGAAGTGGCTGTCTGTGTGGACAGGAAATGGGGTCAACCCCTTTGCTT 1440
QY 1441 CTATCTTGAATCCATCTGGTCAAAATTCAGTGTGAGACCAACCTCAAAACAAAAA 1500
Db 1441 CTATCTTGAATCCATCTGGTCAAAATTCAGTGTGAGACCAACCTCAAAACAAAAA 1500
QY 1501 AGATCTATTCTACTGGATCTGCAGGGAGACAGTGCCTTTTCTGTTCAACAACCTGT 1560
Db 1501 AGATCTATTCTACTGGATCTGCAGGGAGACAGTGCCTTTTCTGTTCAACAACCTGT 1560
QY 1561 TGACTTCCCTGGAAACAGGAGATGGAGAAATTAGGCAAGTGGTCTTTCTAAACTACCGTC 1620
Db 1561 TGACTTCCCTGGAAACAGGAGATGGAGAAATTAGGCAAGTGGTCTTTCTAAACTACCGTC 1620
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QY 1681 CCACTGACATCGTACAGTCTGTAAACAGAAAACCTCTTTGGGACCAATGTGGACA 1740
Db 1681 CCACTGACATCGTACAGTCTGTAAACAGAAAACCTCTTTGGGACCAATGTGGACA 1740
QY 1741 ATGAGTTTTCTCAATAGTACTCTCCACCCCAAGTCTGTAGTGGAGTTTTCTATGTG 1800
Db 1741 ATGAGTTTTCTCAATAGTACTCTCCACCCCAAGTCTGTAGTGGAGTTTTCTATGTG 1800
QY 1801 GCGCTCGGACTTTGGCAAGAGCTCGCAATGCTGTCACGATATTCAGTCTGGATC 1860
Db 1801 GCGCTCGGACTTTGGCAAGAGCTCGCAATGCTGTCACGATATTCAGTCTGGATC 1860
QY 1861 CTAGAAAGGTTCAATCTACTCTTCAACAAAGAAAATTTTGGTTATAGGAATAAGGACGG 1920
Db 1861 CTAGAAAGGTTCAATCTACTCTTCAACAAAGAAAATTTTGGTTATAGGAATAAGGACGG 1920
QY 1921 TAACTCGAATTTGTCTCTTTGTATCTTCAGTAATTTAGTTATAGGAATAAGGACGGTAA 1980
Db 1921 TAACTCGAATTTGTCTCTTTGTATCTTCAGTAATTTAGTTATAGGAATAAGGACGGTAA 1980
QY 1981 TCTGCAATTTGTCTCTTTGTATCTTCAGTAATTTAGTTATAGGAATAAGGACGGTAA 2040
Db 1981 TCTGCAATTTGTCTCTTTGTATCTTCAGTAATTTAGTTATAGGAATAAGGACGGTAA 2040
QY 2041 CACTTTAGGATTAAGATGTGCTCTCAAGCCCTGACTCCCTGGTATTTCTTTTGTATG 2100
Db 2041 CACTTTAGGATTAAGATGTGCTCTCAAGCCCTGACTCCCTGGTATTTCTTTTGTATG 2100
QY 2101 CATTGAACTTGGTACTTGGCTTACGAACTTAAGAACTTCTGAAAGTTCTTAAAGTTCT 2160
Db 2101 CATTGAACTTGGTACTTGGCTTACGAACTTAAGAACTTCTGAAAGTTCTTAAAGTTCT 2160
QY 2161 GAANTTCTTAAAGCCCATGATCTTCTCAGAAAATACTGTAATCTTTCTGGACAG 2220
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QY 2221 CCATGACTGTAGCAAGGCTTTGATAGCAAGTTTGGTGGTTCANAAATATACAATATC 2280
Db 2221 CCATGACTGTAGCAAGGCTTTGATAGCAAGTTTGGTGGTTCANAAATATACAATATC 2280
QY 2281 CCAGGTGATTTTATCAANTCCAGTGTACCATCTCTCGAGTTTGGTTGTGAATCTTTTG 2340
Db 2281 CCAGGTGATTTTATCAANTCCAGTGTACCATCTCTCGAGTTTGGTTGTGAATCTTTTG 2340
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Db 2341 TCCTCCCTCCACCCCAACAGAGATTTTAAGTAGGGTGACTTTTAAATAAAAAATTTATTGA 2400
QY 2401 ATAATTAATGATAAACAATAATAATAAACAATAATAAACAATAATAAACAATAAACA 2460
Db 2401 ATAATTAATGATAAACAATAATAATAAACAATAATAAACAATAATAAACAATAAACA 2460
QY 2461 ATCCCATATAACACCAACAGTGATCATGTTTACTGTCTCACTTTTGATATGTTTATCCAG 2520
Db 2461 ATCCCATATAACACCAACAGTGATCATGTTTACTGTCTCACTTTTGATATGTTTATCCAG 2520
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Db 2521 TGTGAACAGCAATTTATTATTTTGTCTCATCAAAAAATAAAGGATTTTTTTCACITGAA 2580
QY 2581 AAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 2609
Db 2581 AAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 2609
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RESULT 9

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US-10-318-906A-22
; Sequence 22, Application US/10318906A
; Publication No. US20030157678A1
; GENERAL INFORMATION:
; APPLICANT: Lambeth, J. David
; APPLICANT: Griendling, Kathy
; APPLICANT: Lassegue, Bernard
; APPLICANT: Arnold, Rebecca S.
; APPLICANT: Cheng, Guangjie
; TITLE OF INVENTION: Mitogenic Oxygenases
; FILE REFERENCE: 05501-0221
; CURRENT APPLICATION NUMBER: US/10/318,906A
; PRIOR FILING DATE: 2002-12-13
; PRIOR APPLICATION NUMBER: US 09/437,568
; PRIOR FILING DATE: 1999-11-10
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 22
; LENGTH: 2577
; TYPE: DNA
; ORGANISM: Rat
US-10-318-906A-22
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Query Match 50.0%; Score 1305; DB 15; Length 2577;
Best Local Similarity 83.4%; Pred. No. 0;
Matches 1495; Conservative 0; Mismatches 295; Indels 3; Gaps 1;
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QY 132 CTGAAGGACCTCTCCAGAAATCCGAGTTGCTGAATCTTCCCTGTGCTAGAAAGGGCTCCA 191
Db 53 CAGAAAGTTCTCTATCTGGAAGATCCCATCAGAGAAACAGATTGCTCTTAAGAGGCTCCA 112
QY 192 AACCACTCTTGACAAATGGGAACTGGTGGTTAACCTAGTGTTCAGTTTGTTCG 251
Db 113 GACCTCCAAATTTGACAAATGGGAACTGGTGGTTAACCTAGTGTTCAGTTTGTTCG 172
QY 252 GTTGTGTTGGTAGGCTGAAATGTTTTCTGTTTGGTATGCCCTCTGAAATATCAGAG 311
Db 173 GTTCTTGGTGGGCTGAAACATTTTTCGTTTGTAGCTTCTCTGAATATAGAGAG 232
QY 312 GCCGCAAAATACTACTACACAAGAAAAATCCCTGGGTCAACATTTGGCTGTGCCGAGCG 371
Db 233 TCTGACAAAGTACTATTACACGAGAGAAATTCGGAACCTGCCCTTGGCCAGACA 292
QY 372 TCTGCTCTCTGCTGAAATTTTAAACGACCGTGTATCTCTGCTTCTGTTGTGCGCAATCTG 431
Db 293 TCTGCTTGTGCTGAAATTTTAAACAGCATGTTGATCTCTGATTCCTGTGTGTCGAAATCTG 352
QY 432 CTGTCCTTCTGAGGGGACCTGCTCATTTTGCAGCCGACACACTGAGAAAGCAATTTGAT 491
Db 353 CTCTCTTCTGAGGGGACCTGCTCATTTTGCACCAACACGCTGAGAAAGCCATTTGAT 412
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Qy	492	CACAACCTCACCTTCCTCCAAAGCTGGTGGCCCTATATGATCTGGCTCTACATACAGCTATATTCAC	551
Db	413	CACAACCTCACCTTCCTCCAAAGCTGGTGGCCCTATATGATCTGGCTCTACATACAGCTATATTCAC	472
Qy	552	ATCATTCGACACACGTGTTTAACTTTTGACTGTATAGCAGAGCCGACGAGCCACAGATGCG	611
Db	473	ATCATTCGACATCTATTTTAACTTTTGAACGCTACAGTAGAACCCACAGGCCATGGATGGA	532
Qy	612	TCCCTTGCCCTCCATTTCTCCAGCCTATCTCATGATGAGAAAAAGGGGGTTCCTGGCTA	671
Db	533	TCTCTTGCCCTCTGTCTCTCCAGCCTATTCATCCCGAGAAA--GAAGATTCTTGCTGA	589
Qy	672	AATCCCATCCAGTCCCGAAACAACGACAGTCGGAGTATGTGACATTCACACGCTGGCTGGT	731
Db	590	AATCCCATCCAGTCTCCAAACGTCACAGTGATGTATGCAGCATTTACCGATGATTTGCTGGC	649
Qy	732	CTCACTGGAGTGATCATGACAAATAGCCCTTGATTCTCATGGTAACTTCAGCTACTGAGTTTC	791
Db	650	CTTACTGGAGTGGTCGCCACTGTGGCTTTTGGTTCTCATGTGTAACTTCAGCTATGGAGTTT	709
Qy	792	ATCCGGAGGAGTATTTTGAAGTCTTCTGGTATACTCACACCTTTTATCTTCTATATTC	851
Db	710	ATCCGGCAGGAATATTTTGAAGTCTTCTGGTATACACATCACCTTTTCACTCATATTC	769
Qy	852	CTTGCGCTTAGGGAATTCACGGCATTTGGTGGAAATGTCCGGGGTCAAAACAGAGGAGAGCATG	911
Db	770	ATCTGCTTAGGATCCATGGCTCGGGGGGATGTTCCGGGGTCAACACAGAGAGAGCATG	829
Qy	912	AATGAGAGTCACTCCGCAAGTGTGCAGAGTCTTTTGAGATGGGAGATGATCTGACTCC	971
Db	830	AGTGAAGAGTCATCCCGCAACTGTTTCTATCTCTTTCCACGAGTGGGATAGTATGAAAGG	889
Qy	972	CACGTGAGGCGCCCTAAGTTTGAAGGCATCCCCCTCAGTCTTGGAGTGGATCCTTGCA	1031
Db	890	AGTTGCAGAGTCTCTATTTTGTGGGGCAACCCCTCAGTCTTGGAAAGTGGATCCTCGCG	949
Qy	1032	CCGGTCAATCTTTATATCTGTGAAGAGTCTCCGGTTTACCGCTCCACGACGAGAAGTT	1091
Db	950	CCGATTGCTTTTATATCTTTGAAGAGTCTCTCGCTTTTATCGTCCCGGCAGAAAGTCT	1009
Qy	1092	GTGATTACCAAGGTGTGTATCGACCCATCCAAAGTTTGGAAATGCGATGACAGACAGCGT	1151
Db	1010	GTGATTACCAAGGTGTGTATCGACCCATCCAAAGTTTGGAAATGCGATGACAGACAGCGG	1069
Qy	1152	GGCTTCAGCATGGAAGTGGGCGAGTATCTTTGTTAAATTGCCCTCAATCTCTCTCCTG	1211
Db	1070	GGCTTTACTATGGGAATAGGACAGTATATTTCTGTAATTTGCCCTCTCGATTTCTCTCCTG	1129
Qy	1212	GAATGGCATCTTTTATCTTTGACCTCTGCTCCAGAGGAAGATTTCTTCTCCATTCATATC	1271
Db	1130	GAATGGCATCTCTTTACTCTGACCTCTGCTCCAGAGGAAGATTTTCTCCATTCATATTT	1189
Qy	1272	CGAGCAGCAGGGGACTGCACAGAAAACTCATAAAGGCTTTCGAAACAACAATATTCACCA	1331
Db	1190	CGAGCAGCAGGGGACTGCACAGAAAACTCATAGGACATTTGAAACAGAGACTCACCA	1249
Qy	1332	ATTCOCAGGATGGAAGTGGATGGTCCCTTTGGCAACGCGAGTGGAGATGTTTCCAGTAT	1391
Db	1250	ATGCCCAGGATCGAGGTGGATGGTCCCTTTGGCACAGTCAGTGGAGGATGCTTCCAGTAC	1309
Qy	1392	GAAGTGGCTGTGCTGGTTGGAGCAGGAATGGGGTCAACCCCTTGCTCTTACTTTGAAA	1451
Db	1310	GAAGTGGCTGTACTGGTTGGGGCAGGAATGGCGTCACTCCCTTGTCTTCTCTTGA	1369
Qy	1452	TCCATCTGGTCAAAATTCAGTGTGCAGACCACCAACCTCAAACAACAAAAAGATCTATTTTC	1511
Db	1370	TCTATCTGTTCAAAATTCAGCGTGCACACAACAAGCTGAAAAACAAAAAGATCTATTTTC	1429
Qy	1512	TACTGGATCTGCGGAGACAGGTGCCCTTTTCTGGTTTCAACCACTGTTGACTTCCCTG	1571
Db	1430	TACTGGATTTGTAGAGACAGCGGTGCCCTTTGCTGGTTTCAACCACTTATTTGAATTCCTG	1489
Qy	1572	GAACAGGAGATGGAGGAATATAGGCAGAAAGTGGGTTTCTTAAACTACCGTCTCTTCCCTCACC	1631

RESULT 10

US-10-319-236A-22

: Sequence 22. Application US/10319236A

Publication No. US20030165198A1

: PUBLICATION NO: 0320
: GENERAL INFORMATION:

APPLICANT: Lamberth, J. David

APPLICANT: GRIEDLING, KATHY

APPLICANT: GILBERT, KATHY
APPLICANT: LASSEQUE, BERNARD

APPLICANT: Lassegue, Bernard
APPLICANT: Arnold, Rebecca S

APPLICANT: ALHOLD, REDECCA

APPLICANT: Cheng, Guangjie
TITLE OF INVENTION: Antibodies to Mitogenic Oxidases

FILE REFERENCE: 05501-0320 (42150-281176)

FILE REFERENCE: 05501-0220 (43150-2811/6)
CURRENT IDENTIFICATION NUMBER: HC/10/218 2362

; CURRENT APPLICATION NUMBER: US/1
CURRENT FILING DATE: 2002-12-12

;
CURRENT FILING DATE: 2002-12-13

; PRIOR APPLICATION NUMBER: US

; PRIOR FILING DATE: 1999-

; NUMBER OF SEQ ID NOS: 61

; SOFTWARE: Pate

; SEQ ID NO 22

; LENGTH: 2

; TYPE: DNA

; ORGANISM: Rat

Query Match	50.0%	Score 1305;	DB 15;	Length 2577;
Best Local Similarity	83.4%;	Pred. No. 0;		
Matches 1495;	Conservative	0;	Mismatches 295;	Indels 3;
Gaps 1;				

QY	132	CTGAAGGACCTCTCCAGAAATCGGATTCGTGAATCTTCCCTGTGCCTTAGAAGGCTCCA	191
DB	53		
QY	192	AACACACCTCTTCAAAATCGGAAAACTGGGTGGTTAAACCACTGGTCTTTTCAGTTTGTGTTCTG	251
DB	113		
QY	252	GTTGTTTGGTTAGGCTGGAATGTTTTCTGTTTGTGGATGCTTCTCTGAATATATGAGAAG	311
DB	173		
QY	312	GCCGACAAATACTACTACACAAGAAAAATCCTTGGGTCAACAAATGGCCCTGTGCCCGAGCG	371
DB	233		
QY	372	TCTGCTCTCTGCTTGGAATTTTAAAGACGCGTGATCTCTGCTTCTGTGTGTGTCGCAATCTG	431
DB	293		
QY	432	CTGTCTCTTCTCTGAGGGGCACTGCTGTCAATTTTTCAGCCGCGCACACTCGAAGAAGCAATTTGGAT	491

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Db 353 |||||CTCTCTCTGAGGGCAGCTGCTCAATTTGGCAACACACGCTGAGAAAGCCATTGGAT 412
QY 492 CACAACTCCACCTTCCACAAAGCTGGTGGCCCTATATGATCTGCTCATACATACAGCTATTTCAC 551
Db 413 CACAACTCCACCTTCCATAGCTGGTGGCATATATGATCTGCATATTCACAGCTATTTCAT 472
QY 552 ATCAATTGCACACCTGTTTAACTTTGACTGTCTATAGCAAGAGCCGACAGGCCACAGATGGC 611
Db 473 ATCAATTGCACATCATTTTAACTTTGAACGCTACAGTAGAAGCCAAACAGGCCATGATGGA 532
QY 612 TCCCTTTGCCCTCCATCTCTCCAGCTATCTCATGATGAGAAABAGGGGGTCTTCGGCTA 671
Db 533 TCTCTTGGCCCTGTTCTCTCCAGCTATTCCATCCCGAGAAA---GAAGATTTCTTGGCTA 589
QY 672 AATCCCATCCAGTCCCGAAACACGACAGTAGTGAGATGTGACATTCACACAGCGTTGCTGGT 731
Db 590 AATCCCATCCAGTCTCCAAACGTTGACAGTGTATGACGATTTACCAAGTATTTGCTGGC 649
QY 732 CTCACTGGAGTGATCATGACAAATAGCTTGAATCTCATGTGTAATCTCAGCTACTGAGTTC 791
Db 650 CTTACTGGAGTGTGCCCACTGTGGCTTTGGTTCTCATGTGTAATCTCAGCTATGAGATT 709
QY 792 ATCCGGAGGAGTTATTTTGAAGTCTTCTGTGTATCTACACACCTTTTATCTTCTATATC 851
Db 710 ATCCGGAGGAGTTATTTTGAAGTCTTCTGTGTATCTACACACCTTTTATCTTCTATATC 769
QY 852 CTTGGCTTAGGATTCACGGCAATGTGGAAATGTCCGGGGTCAAAACAGAGAGAGCATG 911
Db 770 ATCTGCTTAGGATTCATGCCCTGGGGGATGTCCGGGGTCAAAACAGAGAGAGCATG 829
QY 912 AATGAGTGCATCTCCGAGTGTGACAGTCTTTTGAAGTGTGGAGTGGATGATCTGATCC 971
Db 830 AGTGAAGTGCATCCCGCAACTGTTTCATATCTCTTCCAGAGTGGGTAAGTATGAAGG 889
QY 972 CACTGTAGGCGCCCTAAAGTTGAAGGCGATCCCGCTGAGTCTTGGAGTGGATCCTTGA 1031
Db 890 AGTTGAGGAGTCTCATTTTGGGGCAACCCCTGAGTCTTGGAGTGGATCCTCGCG 949
QY 1032 CGGTCATTTCTTATATCTGTGAAGGATCCTCCGGTTTTACCGCTCCCGCAGAGAGGTT 1091
Db 950 CGGATGTCTTTTATATCTTGAAGGATCCTTCGCTTTTATCGCTCCCGCAGAGGTC 1009
QY 1092 GTGATTACCAAGTTGTTATGACCCATCCAAAGTTTTTGAATGTGAGATGAACAGGCT 1151
Db 1010 GTGATTACCAAGTTGTCATGACCCATGTAAGTTTTTGAATGTGAGATGAGGAAGCGG 1069
QY 1152 GGCTTCAGCATGGAAGTGGGGAGTATATCTTTGTTAATTTGGCCCTCAATCTCTCCCTG 1211
Db 1070 GGCTTTACTATGGGATAGGACAGTATATTCGTAATTTGCCCTCGATTTCCCTTCCTG 1129
QY 1212 GAATGGATCTTTTACTTTGACCTCTGCTCCAGAGGAAGATTTCTTCTCCATTCATATC 1271
Db 1130 GAATGGATCTTTTACTCTGACCTCTGCTCCAGAGGAAGATTTTCTCCATTCATAT 1189
QY 1272 CGAGCAGAGGGGACTGGACAGAAATCTCATAGGCTTTGAAACAAATATTCACCA 1331
Db 1190 CGAGCAGAGGGGACTGGACAGAAATCTCATAGGACATTTGAAACAAACAGCACTCACCA 1249
QY 1332 ATTCCAGGATTTGAAGTGGATGGTCCCTTTGGCAGAGCCAGTGGAGATTTTCCAGTAT 1391
Db 1250 ATGCCCAGGATCGAGTGGATGGTCCCTTTGGCAGTGGAGATGTCTTCAGATAC 1309
QY 1392 GAAGTGGCTGTGCTGGTGGAGAGGAATTTGGGGTCAACCCCTTTGCTTCTATCTTGA 1451
Db 1310 GAAGTGGCTGTACTGGTTGGGGCAGGGAATGGCGTCACTCCCTTTGCTTCTTGA 1369
QY 1452 TCCATCTGTAACAATTCAGTGTGACACCAACACCTCAAAACAAAAGATCTATTTC 1511
Db 1370 TCTATCTGTAACAATTCAGGCTGACACAAAGCTGAAACACAAAAGATCTATTTC 1429
QY 1512 TACTGGATCTGAGGGAGACAGTGCCTTTTCTGGTTCAACAACTGTGTGACTTCCCTG 1571
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Db 1430 TACTGGATTTGTAGAGAGCGGGTGCTTTTGCCTGGTTCAACAACATTATTGAATTCCTG 1489
QY 1572 GAAACAGAGATGAGGAAATTTAGGCAAAAGTGGGTTTTCTTAAACTACCGTCTCTTCTCAC 1631
Db 1490 GAAACAAGATGAGCAAAATTTAGGCAAAACCGGATTTCTTAAACTACCGACTCTTCTCAC 1549
QY 1632 GGATGGGACAGCAATATTTGTGTCATGAGCAATTAACCTTTTGAAGGCCACTGCATC 1691
Db 1550 GGCTGGGATAGCAACATTTGCTGTCATGAGCAATTAACCTTTTGAAGGCCACTGCATC 1609
QY 1692 GTGACAGGTTCTGAAACAGAAACCTCTCTTTGGAGACCAATGTGGGACCAATGATTTCT 1751
Db 1610 CTGACAGGTTCTGAAACAGAAACCTCTCTTTGGAGACCAATGTGGGACCAATGATTTCT 1669
QY 1752 ACAATAGCTACCTCCCAACCCCAAGTCTGTAGTGGGAGTTTTCTTATGTGSCCTCCGACT 1811
Db 1670 AGNATAGCTACTGCCCAACCCCAAGTCTGTGTGGGGTTTTCTTATGTGSCCTCCGACT 1729
QY 1812 TTGGCAAGAGCTGCGCAAAATGTCTCACCGATATTTCCAGTCTGGATCCTAGAAAGTT 1871
Db 1730 TTGGCAAAAGCTGCGCAAAATGTCTGCGCGTACTCAAGTCTGGATCCTAGAAAGTT 1789
QY 1872 CAATTCTACTTCAACAAAGAAATTTTTCAGTTATAGGAATAGGACGGTAAT 1924
Db 1790 CAATTCTACTTCAACAAAGAAACGTTCTGATTTGGAGGAAGCGGCACAGTAGT 1842
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RESULT 11

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US-10-318-906A-41
; Sequence 41, Application US/10318906A
; Publication No. US20030157678A1
; GENERAL INFORMATION:
; APPLICANT: Lambeth, J. David
; APPLICANT: Griendling, Kathy
; APPLICANT: Lassegue, Bernard
; APPLICANT: Arnold, Rebecca S.
; APPLICANT: Cheng, Guangjie
; FILE OF INVENTION: Mitogenic Oxygenases
; FILE REFERENCE: 05501-0221
; CURRENT APPLICATION NUMBER: US/10/318,906A
; CURRENT FILING DATE: 2002-12-13
; PRIOR APPLICATION NUMBER: US 09/437,568
; PRIOR FILING DATE: 1999-11-10
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 41
; LENGTH: 2619
; TYPE: DNA
; ORGANISM: Rat
US-10-318-906A-41
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Query Match 45.3%; Score 1182.8; DB 15; Length 2619;
Best Local Similarity 84.8%; Pred. No. 1.7e-291;
Matches 1338; Conservative 0; Mismatches 237; Indels 3; Gaps 1;

QY 347 GTCAACATTTGGCTGTGCCCGAGCGTCTGCTCTCTGTTGAATTTTAAACAGCACGCTGAT 406
Db 310 GACTGCCTTGGCTTGGCCAGAGCATCTGCTTGTGCTGATTTTAAACAGCATGGTAT 369
QY 407 CTTGCTTCTGTGTGTCGAATCTGCTCTCTTCTGAGGGGACCTGCTCATTTTTCAG 466
Db 370 CTTGATTTCTGTGTGCGAAATCTGCTCTCTTCTGAGGGGACCTGCTCATTTTTC 429
QY 467 CGCACACTGAGAAAGCAATTTGGATCAAACTCACTACCTTCCACAGCTGGTGGCTATAT 526
Db 430 CCACAGCTGAGAAAGCAATTTGGATCAAACTCACTACCTTCCATTAAGCTGGTGGCATATAT 489
QY 527 GATCTGCTACATACAGCTATTTCATCATTCATGCACACCTGTTTAACTTTTGACTGTATAG 586
Db 490 GATCTGCATATTTCAGCTATTTCATATCATTCATGCACATCTTATTAACTTTTGAACGTCAG 549
QY 587 CAGAAAGCGCAGAGGCGACAGATGGTCTCCTTGGCTTCCATCTCTCCAGCCTATCTCATGA 646
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Db 550 TAGAGCCACAGGCGCATGGATGCTCTTGCTCTGTTCTCTCCAGCCATATTCATCC 609
 Qy 647 TGAGAAAAAGGGGGTCTTGGCTAAATCCATCCAGTCCGAAACACGACAGTGAGTA 706
 Db 610 CGAGAAA--GAAGATCTTGGCTAAATCCATCCAGTCCGAAACGACAGTGAGTA 666
 Qy 707 TGTGACATTCACAGCGTCTGGTCTCACTGAGTGATCATGACAAATGCCCTTGATCT 766
 Db 667 TGCAGCAATACAGATGATCTGCGCTTACTGAGTGGTCCGCACTGTGGCTTTGGTTCT 726
 Qy 767 CATGGTAACCTCAGCTACTGAGTTCACTCCGAGAGGATTAATTTGAAGTCTTCTCGTATAC 826
 Db 727 CATGGTAACCTCAGCTACTGAGTTTATCCGAGGAATTAATTTGAGCTCTCTCGTATAC 786
 Qy 827 TCACCACTTTTATCTTATATCTTGTGGTCTAGGATTCACGGCAATGGTGGAAATGT 886
 Db 787 ACATCACTTTTATCATCTATATCATCTCTGTTAGGATCCATGGCCCTGGGGGGATGT 846
 Qy 887 CCGGGTCAACAGAGAGAGCATGAATGAGATCATCTCCGCAAGTGTGCAGAGTCTTT 946
 Db 847 CCGGGTCAACAGAGAGAGCATGAATGAGATCATCTCCGCAAGTGTGTCACTCTTT 906
 Qy 947 TGAGATGGGGATGATCGTGAATCCCACTGAGCGCCCTAAGTTTGAAGGGCATCCCCC 1006
 Db 907 CCAGAGTGGGATAAGTATGAAGGAGTTCAGGAGTCTCATTTTGTGGGCAACCCC 966
 Qy 1007 TGAGTCTTGAAGTGGATCTTGGACCGGTCAITCTTTTATATCTGTGAAGGATCCCG 1066
 Db 967 TGAGTCTTGAAGTGGATCTTGGACCGGTCAITCTTTTATATCTGTGAAGGATCCCG 1026
 Qy 1067 GTTTTACCGCTCCAGAGAGAGTGTGATTAACCAAGTGTGTATGACCCATCCAAAGT 1126
 Db 1027 CTTTATGCTCCCGAGAGAGTGTGATTAACCAAGTGTGTATGACCCATCCAAAGT 1086
 Qy 1127 TTTGGAATGAGATGAACAGCGTGGCTTCAGCATGGAAGTGGGGCAGTATATCTTTGT 1186
 Db 1087 TTTGGAATGAGATGAACAGCGGCTTTACTATGGAATGAGCAGTATATATCTTTGT 1146
 Qy 1187 TAATGGCCCTCAATCTCTCTGGAATGGAATGGAATGGAATGGAATGGAATGGAAT 1246
 Db 1147 AAATGGCCCTCAATCTCTCTGGAATGGAATGGAATGGAATGGAATGGAATGGAAT 1206
 Qy 1247 GGAAGATTTCTTCTCCATTCATATCCAGAGAGAGGAGTGGACAGAAATCTCAATAG 1306
 Db 1207 GGAAGATTTCTTCTCCATTCATATCCAGAGAGAGGAGTGGACAGAAATCTCAATAG 1266
 Qy 1307 GGCTTTGAAACAAATATTCACCAATTCAGAGATGAAGTGGATGCTCCCTTTGGAC 1366
 Db 1267 GACATTTGAAACAAAGCACTCACCAATGCCAGGATCGAGTGGATGGTCTTTGGAC 1326
 Qy 1367 AGCCAGTGAAGATCTTTCCAGTATGAATGGCTGTGCTGGAGCAGGAATGGGT 1426
 Db 1327 AGTCAGTGAAGATCTTTCCAGTATGAATGGCTGTGCTGGAGCAGGAATGGGT 1386
 Qy 1427 CACCCCTTTCTCTATCTTGAATCCATCTGGTACAAATTCAGATGTGCAGACCAAA 1486
 Db 1387 CACTCCCTTTCTCTTGAATCTATCTGTACAAATTCAGATGTGCAGACCAAA 1446
 Qy 1487 CCTCAAAACAAAAGATCTATTTCTACTGATCTGAGGAGAGCAGTGTCTTTCTG 1546
 Db 1447 GCTGAAACACAAAAGATCTATTTCTACTGATTTGTAGAGAGCGGGTGTCTTTG 1506
 Qy 1547 GTTCAACAACTGTGTCTTCCCTGGAAACAGAGATGGAGAAATTAGCAAGTGGT 1606
 Db 1507 GTTCAACAACTGTGTCTTCCCTGGAAACAGAGATGGAGAAATTAGCAAGTGGT 1566
 Qy 1607 TCTAACTACCGTCTCTTCTTCCCGGATGGGACAGCAATATTTGTGTCTATGAGCAT 1666
 Db 1567 CTTAACTACCGTCTCTTCTTCCCGGATGGGACAGCAATATTTGTGTCTATGAGCAT 1626
 Qy 1667 AAATTTGAGAGGCACTGATGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGT 1726
 Db 1627 AAATTTGAGAGGCACTGATGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGT 1686

Qy 1727 ACCAATGTGGCAATGAGTCTTCTCAATAGTCTCTCCACCCCAAGTCTGTAGTGG 1786
 Db 1687 ACCAATGTGGCAATGAGTCTTCTCAATAGTCTCTCCACCCCAAGTCTGTAGTGG 1746
 Qy 1787 AGTTTTCTTATGTGGCCCTCGAGCTTTGGCAAGAGAGCTCGCAAAATGCTGTCAACGATA 1846
 Db 1747 GGTTTCTTATGTGGCCCTCGAGCTTTGGCAAGAGAGCTCGCAAAATGCTGTGCGGATA 1806
 Qy 1847 TTCAGTCTGGATCTCTAGAAAGTTCATTTCTACTTCAACAAAGAAATTTTGAAGTAT 1906
 Db 1807 CTCAGTCTGGATCTCTAGAAAGTTCATTTCTACTTCAACAAAGAAACGTTCTGAATGG 1866
 Qy 1907 AGGAATGAAGACGTAAT 1924
 Db 1867 AGGAAGCCGACAGTAGT 1884
 RESULT 12
 US-10-319-236A-41
 ; Sequence 41, Application US/10319236A
 ; Publication No. US20030166198A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Lambeth, J. David
 ; APPLICANT: Griending, Kathy
 ; APPLICANT: Lassegue, Bernard
 ; APPLICANT: Arnold, Rebecca S.
 ; APPLICANT: Cheng, Guangjie
 ; TITLE OF INVENTION: Antibodies to Mitogenic Oxygenases
 ; FILE REFERENCE: 05501-0220 (43150-281176)
 ; CURRENT APPLICATION NUMBER: US/10/319,236A
 ; CURRENT FILING DATE: 2002-12-13
 ; PRIOR APPLICATION NUMBER: US 09/437,568
 ; PRIOR FILING DATE: 1999-11-10
 ; NUMBER OF SEQ ID NOS: 61
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 41
 ; LENGTH: 2619
 ; TYPE: DNA
 ; ORGANISM: Rat
 ; US-10-319-236A-41
 Query Match 45.3%; Score 1182.8; DB 15; Length 2619;
 Best Local Similarity 84.8%; Pred. No. 1.7e-291;
 Matches 1338; Conservative 0; Mismatches 237; Indels 3; Gaps 1;

Qy 347 GTCAACATTTGGCTGTGGCCGAGGCTGTCTCTGCTGAAATTTTAAACAGCAGCTGAT 406
 Db 310 GACTGCTTTGGCTTTGGCCAGAGCATCTGCTTTGCTGCTGAAATTTTAAACAGCAGCTGAT 369
 Qy 407 CCTGCTTCTGTGTGTCGCAATCTGCTCTCTGAGGGGACCTGCTCATTTTTCAG 466
 Db 370 CCTGATTTCTGTGTGTCGCAATCTGCTCTCTGAGGGGACCTGCTCATTTTTCAG 429
 Qy 467 CCGCACACTGAGAAAGCAATTTGGATCAACCTCACCTTCCAAAGCTGGTGGCTATAT 526
 Db 430 CCACAGCTGAGAAAGCAATTTGGATCAACCTCACCTTCCAAAGCTGGTGGCTATAT 489
 Qy 527 GATCTGCTATACACAGTATTCATCATATTCGACACTGTTTAACTTTGACTGCTATAG 586
 Db 490 GATCTGATATTCACAGTATTCATCATATTCGACACTGTTTAACTTTGAACTGCTATAG 549
 Qy 587 CAGAAAGCCGACAGATGCTCCCTGCTCCATCTCTCCAGCCCTATCTCATGA 646
 Db 550 TAGAAGCCACAGCCATGGATGATCTTTGCTCTGTTCTCTCCAGCTATTTCCATCC 609
 Qy 647 TGAGAAAAAGGGGTCTTGGCTTAAATCCATCCAGTCCCGAAACACAGCAGTGGAGTA 706
 Db 610 CGAGAAA--GAAGATTTCTGGCTAAATCCCATCCAGTCTCCAAACGTSACAGTATGTA 666
 Qy 707 TGTGACATTCACAGCGTGTGCTGCTCACTGGAGTATCATCAATAGCTTGTATCT 766
 Db 667 TGCAGCATTTTACAGTATTTGCTGCTTACTGGAGTGGTCCCACTGTGGCTTTGGTTCT 726

QY 767 CATGGTAACCTCAGCTACTGAGTTTCATCCGAGAGATTATTTTGAAGTCTCTTGGTATAC 826
Db 727 CATGGTAACCTCAGCTACTGAGTTTCATCCGAGAGATTATTTTGAAGTCTCTTGGTATAC 786
QY 827 TCACCAACCTTTTATCTCTTATATCTTGTGCTTAGGGATTCACGGCAATTGGTGAATTGT 886
Db 787 ACATCACTTTTTCATCATCTATATCATCTGCTTAGGGATCCATGGCTGGGGGGGATTGT 846
QY 887 CCGGGTCAACAGAGAGAGAGCATGAATGAGAGTCATCTCGCAAGTGTGCAGAGTCTTT 946
Db 847 CCGGGTCAACAGAGAGAGAGCATGAGTGAAGTCATCTCCCGCAACTGTTCTATCTTT 906
QY 947 TGAGATGTGGGATGATCGTGACTCCCACTGTAGCGGCCCTTAAGTTTGAAGGGCATCCCC 1006
Db 907 CCAGAGTGGGATGAAGTATGAAGAGGTTCAGAGAGTCTCATTTTGTGGGGCAACCCCC 966
QY 1007 TGAGTCTTGGAGTGGATCTTGCACCGGTCAATCTTTATATCTGTGAAGAGTCTCCG 1066
Db 967 TGAGTCTTGGAGTGGATCTTGCAGCGGATGCTTTTATATCTTTGAAGAGTCTCTCG 1026
QY 1067 GTTTTACCGTCCAGAGAGGTTGTGATTACCAAGGTTGTATGACCCCATCCAAAGT 1126
Db 1027 CTTTATCGTCCCGCAGAGGTCGTGATTACCAAGGTTGTATGACCCCATGTAAGT 1086
QY 1127 TTTGGAATTGCGAGATGAACAAGCGTGGCTTCAGCATGGAGTGGGCGAGTATCTTTGT 1186
Db 1087 TTTGGAATTGCGAGATGAGGAGCGGGCTTTTACTATGGGAATAGGACAGATATATCGT 1146
QY 1187 TAAATGCCCCCTCAATCTCTCTGGAATGGCATCTTTTACTTTGACCTCTGCTCCAGA 1246
Db 1147 AATATGCCCCCTCGATTTCTCTGATGGCATCCCTTTACTCTGACCTCTGCTCCAGA 1206
QY 1247 GGAAGATTTCTTCTCATTCATATCCAGAGCAGCGGAGTGGACAGAAAACTCATAG 1306
Db 1207 GGAAGATTTTCTTCCATTCATATCCAGAGCAGCGGAGTGGACAGAAAACTCATAG 1266
QY 1307 GCGTTTCGACACACATATTCACCAATTCAGGATTTGAAGTGGATGGTCCCTTGGGAC 1366
Db 1267 GACATTTGAACACACAGCATCCACCAATGCCAGGATCGAGGTGGATGGTCCCTTTGGCAC 1326
QY 1367 AGCCAGTGGAGTGTTTTCCAGTATGAAGTGGCTGTGCTGGTGGAGCAGGAATGGGGT 1426
Db 1327 AGTCAGTGGAGTGTCTTCCAGTACGAAGTGGCTGTGCTGGTGGGAGGAGTGGCGT 1386
QY 1427 CACCCCTTTGCTTCTATCTTGAATTCATCTGGTACAAATTCAGTGTGCAGACCAAA 1486
Db 1387 CACTCCCTTTGCTTCTTGAATTCATCTGGTACAAATTCAGCGTGCACACAA 1446
QY 1487 CCTCAAAACAAAAGATCTATTTCTACTGGATCTGAGAGAGCGGTTGCTTTGCCGTG 1546
Db 1447 GCTGAANAACAAGATCTATTTCTACTGGATTTGTAGAGAGCGGTTGCTTTGCCGTG 1506
QY 1547 GTTCAACAACTGTTGACTTCCCTGGAAACAGAGATGGAGGAATTAGGCAAGTGGTTT 1606
Db 1507 GTTCAACAACTTATTGAATTCCTTGGAAACAGAGATGGAGGAATTAGGCAACCGGATTT 1566
QY 1607 TCTAACTACCGTCTTCTCCTCACCGGATGGGACAGCAATATGTTGGTTCATCGAGCAAT 1666
Db 1567 CTTAACTACCGACTCTTCTCCTCACTGGCTGGATAGCAATGTGGTTCATCGAGCAAT 1626
QY 1667 AAACCTTTCAGAGGCCACTGACATCGTGAAGTCTGAAACAGAAACCTCTTTGGGAG 1726
Db 1627 AAACCTTTCAGAGGCCACTGAGCTCTGACAGGTCTGAAACAGAAACCTCTTTGGGAG 1686
QY 1727 ACCAATGTGGGACAATAGTTTTCTACAAATAGTACTCTCCACCCCAAGTCTGTAGTGGG 1786
Db 1687 ACCAATGTGGGACAATAGTTTTCTAGAAATAGTACTGCCCACCCCAAGTCTGTGGG 1746
QY 1787 AGTTTTCTTATGTGGCCCTCGGACTTTTGGCAAGAGCCTTGGCAAAATGCTGTCACCGATA 1846
Db 1747 GGTTTTCTTATGCGGCCCTCCGACTTTTGGCAAAAGCCTTGGCAAAATGCTGTCGCGGTA 1806

QY 1847 TTCCAGTCTGGATCTCTAGAAAGGTTCAATTTCTACTTCAACAAAGAAAAATTTTTCAGTTAT 1906
Db 1807 CTCAAGTCTGGATCTCTAGAAAGGTTCAATTTCTACTTCAACAAAGAAACGTTCTGAAATGG 1866
QY 1907 AGGAATAAGACGGTAAT 1924
Db 1867 AGGAAGCCGCACAGTAGT 1884

RESULT 13

US-10-618-839-15

; Sequence 15, Application US/10618839

; Publication No. US20040093628A1

; GENERAL INFORMATION:

; APPLICANT: Lambeth, J. David

; APPLICANT: Cheng, Guangjie

; APPLICANT: McCoy, James

; TITLE OF INVENTION: Methods and Transgenic Mouse Model for Identifying and Modulating

; TITLE OF INVENTION: Factors Involved in the Production of Reactive Oxygen

; FILE REFERENCE: 05501-0211 (43150-286808)

; CURRENT APPLICATION NUMBER: US/10/618,839

; CURRENT FILING DATE: 2003-07-14

; PRIOR APPLICATION NUMBER: US 60/395,498

; PRIOR FILING DATE: 2002-07-12

; NUMBER OF SEQ ID NOS: 19

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 15

; LENGTH: 797

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Synthetic primer

US-10-618-839-15

Query Match

Best Local Similarity 30.5%; Score 797; DB 17; Length 797;

Matches 797; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1065 CGGTTTACCGCTCCAGCAGAGGTTGTGATTACCAAGTTGTTATGCAACCATCCAAA 1124
Db 1 CGGTTTACCGCTCCAGCAGAGGTTGTGATTACCAAGTTGTTATGCAACCATCCAAA 60
QY 1125 GTTTTGAATTCAGATGAACAAAGCGTGGCTTCAGCATGGAAGTGGGCGAGTATATCTTT 1184
Db 61 GTTTTGAATTCAGATGAACAAAGCGTGGCTTCAGCATGGAAGTGGGCGAGTATATCTTT 120
QY 1185 GTTAATGGCCCTCAATCTCTCTCTGGAATGGCATTCCTTTTACTTTGACCTCTGCTCA 1244
Db 121 GTTAATGGCCCTCAATCTCTCTCTGGAATGGCATTCCTTTTACTTTGACCTCTGCTCA 180
QY 1245 GAGGAAGATTTCTTCTCCATTCATATCCAGCAGCAGGGGACTGGACAGAAATCTCATA 1304
Db 181 GAGGAAGATTTCTTCTCCATTCATATCCAGCAGCAGGGGACTGGACAGAAATCTCATA 240
QY 1305 AGGGCTTTTGAACAAATATTTTCAATTCAGGATTTGAAGTGGATGGTCCCTTTGGC 1364
Db 241 AGGGCTTTTGAACAAATATTTTCAATTCAGGATTTGAAGTGGATGGTCCCTTTGGC 300
QY 1365 ACAGCAGTGGAGGATTTTCCAGTATGAAGTGGCTGTGCTGGTGGAGCAGGAATGGG 1424
Db 301 ACAGCAGTGGAGGATTTTCCAGTATGAAGTGGCTGTGCTGGTGGAGCAGGAATGGG 360
QY 1425 GTACCCCTTTGCTTCTATCTTGAATCCATCTGGTACAAATCCAGTGTGCAGACAC 1484
Db 361 GTACCCCTTTGCTTCTATCTTGAATCCATCTGGTACAAATCCAGTGTGCAGACAC 420
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Db 481 TGGTTCAACACCTGTTGACTTCCCTGGAACAGAGATGAGGAAATAGGCAAGTGGT 540
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 Qy 1845 TATTCAGTCTGGATCC 1861
 Db 781 TATTCAGTCTGGATCC 797

RESULT 14

US-10-342-887-480
 ; Sequence 480, Application US/10342887
 ; Publication No. US20040058340A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Dai, Hongyue
 ; APPLICANT: He, Yudong
 ; APPLICANT: Linsley, Peter S.
 ; APPLICANT: Mao, Mao
 ; APPLICANT: Roberts, Christopher J.
 ; APPLICANT: Van 't Veer, Laura Johanna
 ; APPLICANT: Van de Vijver, Marc J.
 ; APPLICANT: Bernards, Rene
 ; TITLE OF INVENTION: Diagnosis and Prognosis of Breast Cancer Patients
 ; FILE REFERENCE: 9301-188-999
 ; CURRENT APPLICATION NUMBER: US/10/342,887
 ; CURRENT FILING DATE: 2003-01-15
 ; PRIOR APPLICATION NUMBER: 60/298,918
 ; PRIOR FILING DATE: 2001-06-18
 ; PRIOR APPLICATION NUMBER: 60/380,710
 ; PRIOR FILING DATE: 2002-05-14
 ; PRIOR APPLICATION NUMBER: 16/172,118
 ; PRIOR FILING DATE: 2002-06-14
 ; NUMBER OF SEQ ID NOS: 2699
 ; SEQ ID NO 480
 ; LENGTH: 4266
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-10-342-887-480

Query Match 22.3%; Score 582; DB 13; Length 4266;
 Best Local Similarity 60.0%; Pred. No. 1.6e-137;
 Matches 1035; Conservative 0; Mismatches 665; Indels 24; Gaps 3;
 Qy 204 ACAATGGAACTGGTGGTTTAAACCCTGTTTTCAGTTTGTCTGTTGTTTGGTTA 263
 Db 12 ACCATGGGAACTGGGCTGTGAATGAGGGCTCTCCATTTTGTCAITTCGTGTTGGCTG 71
 Qy 264 GGGCTGAATGTTTTCCTGTTTGTGGATGCCCTTCTGAAATATGAGAGGCCGACAAATAC 323
 Db 72 GGGTTGAACGCTTCCTCTTGTCTGTTATACCGGGTTTATGATATTCACCTAAGTTC 131
 Qy 324 TACTACACAGAAAACTCTTGGTCAAATGTCCTGTCGCGAGCGCTCTGCTCTGTC 383
 Db 132 TTTTACACAGAAAACTCTTGGGTCAGCACTGGCACTGGCGAGGGCCCTGCGACCTGC 191
 Qy 384 TTGAATTTTACGACGCTGATCTGCTTCTGTTGTCGCAATCTGCTGCTCTCTG 443
 Db 192 CTGAATTTCACTGATCTGATCTCTTGGCAGTCTGTGAAATCTGCTGCTCTCTC 251

Qy 444 AGGGCGACCTGCTCAITTTTGCAGCGCACACTGAGAAAGCAATTTGGATCACAACTCAC 503
 Db 252 AGGGTTCACAGTTCGCTGCTCTCAACAGAGTTTGAAGACACTGGACAGATCTCAC 311
 Qy 504 TTCCACAAGCTGTGGCTTATATGATCTGCTACATACAGCTATTTCACTATTCATTCGAC 563
 Db 312 TTTTCAATAATGTGGATGATGATGCTTCACTCTCGGATTCACCAATTCACAT 371
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 Qy 624 ATTTCTCTCCAGCCTATCTCATGATGAGAAAGGGGGTTCTTGGCTAAATCCCATCCAG 683
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 Db 849 CTGTATCTCTGTGAGAGTTTGGTGGGTTTGGGCTCTCAACAGAGGTTGGTCTATCACC 908
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 Db 909 AAGTGGTCACTCAACCTTTCAAAACCATCGAGTACAGATGAAGAGAGGGTTCAAA 968
 Qy 1161 ATGGAAGTGGGCGAGTATATCTTTGTTAAATGCCCCCTCAATCTCTCTCTGGAATGGCAT 1220
 Db 969 ATGGAAGTGGGCAATACATTTTGTCAAGTGCCCAAGGTGTCCAAGCTGAGTGGCAC 1028
 Qy 1221 CTTTATTTTGAACCTCTGCTCAGAGAGAGATTTCTTCTCCATTCATATCCGAGCAGCA 1280
 Db 1029 CTTTATCACTACATCCGCTCCCTGAGGAGAGACTTCTTAGTATCCATATCCGATCGTT 1088
 Qy 1281 GGGGACTGGACAGAAATCTCATAGGCTTTTCG-----AAACACAA 1322
 Db 1089 GGGGACTGGACAGAGGGCTGTTCAATGCTTGTGGTGTGATAAGCAGGAGTTTCAAGAT 1148
 Qy 1323 TATTCAACCAATTTCCAGGATTTGAAGTGGTCCCTTTTGGCAGCGAGTGAAGATGTT 1382
 Db 1149 GCGTGGAAACTTACCTAAGATAGCGGTTGATGGGCTTTTGGCACTGCGCAGTGAAGATGTG 1208
 Qy 1383 TTCAGATATGAATGGCTGTGCTGTTGGAGCAGAAATGGGGTCAACCCCTTGTCTTCT 1442
 Db 1209 TTCAGCTATGAGTGGTGTGATTTAGTGGGAGCAGGATTTGGGGTCAACCCCTTGCATCC 1268
 Qy 1443 ATCTTGAATCCATCTCTGTCACAAATTTCCAGTGTGAGACCAACCAACCTCAAAACAAAAAG 1502
 Db 1269 ATTCTCAAGTCACTGTCGTACAAATATTGCAATTAACGCCCAACCAATCTGAAGCTCAAAAG 1328
 Qy 1503 ATCTATTTCTACTGATCTGAGGAGACAGGTGCTTTTCTGTTTCAACAACTGTTG 1562

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Db 1329 ATCTACTTCTACTGGCTGTGCGGACACACATGCTTGTGAGTGGTTTGCAGATCTGCTG 1388
Qy 1563 ACTTCCCTGGAAACAGAGATGGAGGAATAGGCAAGTGGGTTTCTAAACTACCGTCTC 1622
Db 1389 CAACTGCTGGAGAGCCAGATGCAAGAAAGGAACAATGCGGCTTCTCTCAGCTACAACATC 1448
Qy 1623 TTCTCTACCGGATGGGACAGCAATATTGTTGGTCTATGAGCATGAGCAATAAACTTTGACAAGGCC 1682
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Qy 1743 GAGTTTCTACAATAGTACTCTCCACCCCAAGTCTGTAGTGGAGTTTCTTATGTGGC 1802
Db 1569 GAATTCAAAGCAATGTGAAGTCAACACCCTAATACCAGAATAGGAGTTTCTCTGTGGA 1628
Qy 1803 CCTCGGACTTTGGCAAGAGCCCTGGCAAAATGCTGTACCGATATTCAGTCTGGATCCT 1862
Db 1629 CCTGAAGCCTTGGTGAAACCCCTGAGTAAACAAAGCAATCTCCAACTCTGAGTCTGGCCCT 1688
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Db 1689 CGGGAGTGCATTTCTATTTTCAACAGAAAACTTCTAACTTGT 1732
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RESULT 15

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US-10-172-118-480
; Sequence 480, Application US/10172118
; Publication No. US20030224374A1
; GENERAL INFORMATION:
; APPLICANT: Dai, Hongyue
; APPLICANT: He, Yudong
; APPLICANT: Linsley, Peter
; APPLICANT: Mao, Mao
; APPLICANT: Roberts, Chris
; APPLICANT: Van 't Veer, Laura
; APPLICANT: Van de Vijver, Marc
; APPLICANT: Bernards, Rene
; TITLE OF INVENTION: Diagnosis and Prognosis of Breast Cancer Patients
; FILE REFERENCE: 9301-175-999
; CURRENT APPLICATION NUMBER: US/10/172,118
; CURRENT FILING DATE: 2002-06-14
; PRIOR APPLICATION NUMBER: 60/380,770
; PRIOR FILING DATE: 2002-05-14
; NUMBER OF SEQ ID NOS: 2699
; SEQ ID NO 480
; LENGTH: 4266
; TYPE: DNA
; ORGANISM: Homo sapiens
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: NM 000397
; DATABASE ENTRY DATE: 2001-06-18
US-10-172-118-480
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Query Match 22.3%; Score 582; DB 13; Length 4266;
Best Local Similarity 60.0%; Pred. No. 1.6e-137;
Matches 1035; Conservative 0; Mismatches 665; Indels 24; Gaps 3;

Qy 204 ACAATGGGAAACTGGGTGGTTAAACCACTGGTTTTCAGTTTTTGTCTGTTTGGTTT 263
Db 12 ACCATGGGAACTGGCTGTGATGAGGGCTCTCCATTTTGTCAATCTGTTGGTGTG 71

Qy 264 GGGCTGAATGTTTCTCTGTTTGTGGATGCTTCTTGAATATGAGAAGCCGACAAATAC 323
Db 72 GGGTTGAACGTCTCTCTTTTGTCTGTTATTACCGGTTTATGATATCCACTAAGTTC 131

Qy 324 TACTACAGAAAAAATCTTGGGTCAACATTTGGCTGTGCGCGAGGCTCTCTCTCTGC 383
Db 132 TTTTACAGAAAAAATCTTGGGTGAGCACTGGCACTGGCCAGGCGCCCTCGACGCTC 191
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Qy 384 TTGAATTTTAAACAGCAGCGTGAATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTG 443
Db 192 CTGAATTTTCAACTGCATGCTGATTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTC 251
Qy 444 AGGGGCACTGCTCATTTTTCAGCCGACACTGAGAAAGCAATTTGGATTCACAACTCACC 503
Db 252 AGGGGTTTCCAGTGGCTGCTCTCAACAAGAGTTTGAAGACAACACTGAGCAATCTCACC 311
Qy 504 TTCCACAAGCTGGTGGCTATATGATCTGCTACATACAGCTATTTCACATCATTTGACAC 563
Db 312 TTTTCAATAAATGGTGGATGATTTGCACTTCACTCTCTCTCTCTCTCTCTCTCTCTCAT 371
Qy 564 CTGTTAACTTTTGACTGCTATAGCAAGCCGACAGCCACAGATGCTCTCTCTCTCTCTCT 623
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Qy 624 ATTCTCTCCAGCCTATCTCATGATGAGAAAAAGGGGGTTCTTTGGGTAAATTCACATCCAG 683
Db 432 GCATCTCTGAACTTGGAGACAGGCAAAATGAAAGTTATCTCAATTTTGTCTGAAAGAGA 491
Qy 684 TCCGGAACACAGCAGTGG---AGTATGTGACATTCACACAGCGTTCGTGCTCTCACTGGA 740
Db 492 ATAAAGAACCTTGAAGAGCGCTGTACTGGCTGTGACCTGTTGGCAGGCATCTCTGGA 551
Qy 741 GTGATCATGACAATAGCCTTTGATTTCTCATGGTAACTTCAGCTACTGAGTTTCATCCGAGG 800
Db 552 GTTGTCTATCAGCGTGTGCTCTCATTAATATATCACTTCTCTCCACAAAACCATCCGAGG 611
Qy 801 AGTTATTTTGAAGTCTCTCTGTTATCTCTCACCACCTTTTATCTCTCTATCTCTTGGCTTA 860
Db 612 TCTTACTTGAAGTCTTTTGGTACACATCATCTCTTTTGTGATCTCTTCTTCAATTTGSCCTT 671
Qy 861 GGGATTCAAGCATTTGGTGAATTTGTCGGGGTCAACAGAGGAGAGCATGAATGAGAT 920
Db 672 GCATCTCATGAGCTGAACGAATTTGACTGGCAGACCCGAGAGAGTTTGGCTGTGCAT 731
Qy 921 CATCTCGCAAGTGTGACAGTCTTTTGTGAGATGTGGGATGATCGTGACTCCCACTCTGAGG 980
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Db 789 ATCCCTCAGTTTGTGGAACCCCTCTCTATGATGGAAATGATAGTGGGTCCCATGTTT 848
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Db 849 CTGTATCTCTGTGAGAGGTTGGTGGGTTTGGCGATCTCAACAGAAAGTTGGTTCATCACC 908
Qy 1101 AAGTTTGTATGCACCCATCCAAAGTTTGGAAATTTGCAGATGAACAAGCGTGGCTTCAGC 1160
Db 909 AAGTGGTCACTCAGCCCTTTCAAAACCATCGAGCTACAGATGAAGAAGAGGGTTCAAA 968
Qy 1161 ATGGAAGTGGGCACTATATCTTCTGTTAAATTCGCCCTCAATCTCTCTCTCTGGAATGGCAT 1220
Db 969 ATGGAAGTGGGCAATAATATTTTGTCAAGTCCCAAGGTGTCCAAGCTGAGTGGGCAC 1028
Qy 1221 CTTTTTACTTTGACCTCTGCTCCAGAGGAAGATTTCTTCTCCATTCATATCCGAGCAGCA 1280
Db 1029 CTTTTTACACTGACATCCGCCCTGAGGAAGACTTCTTTAGTATCCATATCCGATCGTT 1088
Qy 1281 GGGGACTGGACAGAGGGGCTGTTCAAATGCTTGTGGCTGTGATAGCAGAGTTTCAAGAT 1322
Db 1089 GGGGACTGGACAGAGGGGCTGTTCAAATGCTTGTGGCTGTGATAGCAGAGTTTCAAGAT 1148
Qy 1323 TATTCACCAATTTCCAGGATTCAGTGTGATGGTCCCTTTGGCAGAGCCAGTGAAGATGTT 1382
Db 1149 GCGTGGAACTACCTTAAGATAGCGGTTGATGGGCCCTTTGGCAGTCCGAGTGAAGATGTG 1208
Qy 1383 TTCCAGTATGAAGTGGCTGTGCTGGTGGAGCAGGAATTTGGGTCACCCCTTTGCTTCT 1442
Db 1209 TTCAGTATGAGTGGTGTGATTTAGTGGAGCAGGATTTGGGTCACACCCCTTGCATCC 1268
Qy 1443 ATCTTGAATTCATCTGTGTCAAAATTTCCAGTGTGAGACCACCAACCTCAAAAACAAAAAG 1502
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Qy	1503	ATCTATTCTTACTGGATCTGCAGGGAGACAGGTGCGCTTTTCTGGTTCAACAACCTGTTG	1562
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Qy	1563	ACTTCCCTGGAAACAGGAGATGGAGGAATTAGGCHAAAGTGGGTTTCTAAACTACCGTCTC	1622
Db	1389	CAACTGCTGGAGAGCCAGATGCAGGAAGGAACAATGCCGCTTCTCAGCTACAACATC	1448
Qy	1623	TTCTCTACCGGATGGGACAGCAATATTGTTGGTCAATGCAGCATTTAAACTTTGACAAGGCC	1682
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Db	1509	AAAGATGTATCACAGGCTTGAACACAAAAGACTTTGTATGAGCGGCCCAACTGGGATAAT	1568
Qy	1743	GAGTTTCTTACAATAGTACTCTCCACCCCAAGTCTGTAGTGGAGTTTCTTATGTGGC	1802
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Db	1629	CCTGAAGCCTTGGCTGAACCCCTGAGTAAACAAGCATCTCCAATCTGAGTCTGGCCT	1688
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Search completed: July 23, 2004, 13:47:58
Job time : 1153 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 23, 2004, 07:28:50 ; Search time 6455 Seconds
(without alignments)
12069.780 Million cell updates/sec

Title: US-10-618-839-1

Perfect score: 2609

Sequence: 1 gctgatagcacagtctgtc.....aaaaaaaaaaaaaaaaaaaaa 2609

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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2: em_esthum:*

3: em_estin:*

4: em_estnu:*

5: em_estcov:*

6: em_estpl:*

7: em_estro:*

8: em_estro:*

9: gb_est1:*

10: gb_est2:*

11: gb_est3:*

12: gb_est3:*

13: gb_est4:*

14: gb_est5:*

15: em_estfun:*

16: em_estom:*

17: em_gss_hum:*

18: em_gss_inv:*

19: em_gss_pln:*

20: em_gss_vrt:*

21: em_gss_fun:*

22: em_gss_mam:*

23: em_gss_mus:*

24: em_gss_pro:*

25: em_gss_rod:*

26: em_gss_pig:*

27: em_gss_vrl:*

28: gb_gsl:*

29: gb_gsl2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
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3	1108.6	42.5	1689	29	AY403532	AY403532 Mus muscu
4	658.6	25.2	668	10	AW850622	AW850622 IL3-CT021

5	644.8	24.7	665	10	AW377012	AW377012 IL3-CT021
6	633.2	24.3	652	10	AW604216	AW604216 IL3-CT021
7	614.8	23.6	618	10	AW850616	AW850616 IL3-CT021
c	614.6	23.6	695	10	AW752752	AW752752 IL3-CT021
9	605.4	23.2	607	10	AW604206	AW604206 IL3-CT021
10	601.8	23.1	618	10	AW850625	AW850625 IL3-CT021
11	597.2	22.9	605	10	AW604209	AW604209 IL3-CT021
12	584	22.4	3242	11	AK053920	AK053920 Mus muscu
13	580.6	22.3	588	10	AW376980	AW376980 IL3-CT021
14	580	22.2	4000	11	BC042838	BC042838 Mus muscu
15	579.8	22.2	583	10	AW850699	AW850699 IL3-CT021
16	577.8	22.1	3925	11	AK033570	AK033570 Mus muscu
17	577.2	22.1	605	10	AW604208	AW604208 IL3-CT021
18	576.8	22.1	592	10	AW604284	AW604284 IL3-CT021
19	559	21.4	559	10	AW604166	AW604166 IL3-CT021
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21	546.4	20.9	564	10	AW376901	AW376901 IL3-CT021
22	545	20.9	561	10	AW752748	AW752748 IL3-CT021
23	541	20.7	541	10	AW376979	AW376979 IL3-CT021
24	536.4	20.6	538	10	AW376866	AW376866 IL3-CT021
c	534.8	20.5	608	10	AW604199	AW604199 IL3-CT021
26	533.8	20.5	545	10	AW376968	AW376968 IL3-CT021
27	527.6	20.2	545	10	AW377061	AW377061 IL3-CT021
c	524.8	20.1	584	13	BQ325148	BQ325148 MR3-CI018
29	512.2	19.6	517	10	AW604210	AW604210 IL3-CT021
30	508.4	19.5	740	10	AW850619	AW850619 IL3-CT021
31	503.2	19.3	510	10	AW377032	AW377032 IL3-CT021
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33	492	18.9	563	10	AW604198	AW604198 IL3-CT021
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c	446.4	17.1	593	9	AI821410	AI821410 ne48a05.x
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ALIGNMENTS

RESULT 1	AY403530	AY403530	1695 bp	DNA	linear	GSS 15-DEC-2003
LOCUS	Homo sapiens NOX1 gene, VIRTUAL TRANSCRIPT, partial sequence,					
DEFINITION	genomic survey sequence.					
ACCESSION	AY403530					
VERSION	AY403530.1					
KEYWORDS	GSS.					
SOURCE	Homo sapiens (human)					
ORGANISM	Homo sapiens					
REFERENCE	1 (bases 1 to 1695)					
AUTHORS	Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarawal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.					
TITLE	Inferring nonneutral evolution from human-chimp-mouse orthologous gene trios					
JOURNAL	Science 302 (5652), 1960-1963 (2003)					
PUBMED	14671302					
REFERENCE	2 (bases 1 to 1695)					
AUTHORS	Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarawal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.					
TITLE	Direct Submission					

JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA

COMMENT This sequence was made by sequencing genomic exons and ordering
them based on alignment.

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Location/Qualifiers
source 1..1695
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
<1..>1695
/gene="NOX1"
/locus_tag="HCM1588"

ORIGIN

Query Match 55.7%; Score 1454.4; DB 29; Length 1695;
Best Local Similarity 85.8%; Pred. No. 6.1e-212;
Matches 1455; Conservative 0; Mismatches 240; Indels 0; Gaps 0;

Qy 207 ATGGGAAATCGGTGGTTAAACACTGGTTTTCAGTTTTCGTGTTGTTGGTTAGG 266
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Qy 327 TACACAGAAATTCCTGGGTCAACATTGGCTGTGCCGAGCGTCTCTCTGCTGTG 386
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Qy 387 AATTTTAAACAGCAGCTGATCCTGTCTCTGTGTGCGCAATCTGCTGCTTCTGTAGG 446
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QY 1887 AAAGAAAATTTTGA 1901
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 ACCESSION AY403532
 VERSION AY403532.1 GI:39759515
 KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus

REFERENCE
 AUTHORS Mammalia; Chordata; Craniata; Vertebrata; Euteleostomi;
 Eukaryota; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 1689)
 Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A.,
 Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,
 Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J.,
 Adams, M.D. and Cargill, M.
 Adams, M.D. and Cargill, M.
 Inferring nonneutral evolution from human-chimp-mouse orthologous
 gene trios

TITLE
 Science 302 (5652), 1960-1963 (2003)
 14671302

JOURNAL
 PUBLISHED 2 (bases 1 to 1689)
 Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A.,
 Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,
 Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J.,
 Adams, M.D. and Cargill, M.

REFERENCE
 AUTHORS Direct Submission
 Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
 Rockville, MD 20850, USA
 This sequence was made by sequencing genomic exons and ordering
 them based on alignment.

COMMENT
 Location/Qualifiers

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 Matches 1254; Conservative 0; Mismatches 435; Indels 6; Gaps 2;

QY 207 ATGGAAACTGGTGTAAACACTGGTTTCAGTTTGTCTGTTGTTGGTTAGG 266
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QY 267 CTGAATGTTTCTGTTTGTGATGCTTCTCTGAAATATGAGAGCGCGACAAATCTAC 326
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DEFINITION AW850622
ACCESSION AW850622
VERSION AW850622.1 GI:7946139
KEYWORDS EST.
SOURCE Homo sapiens
ORGANISM Homo sapiens (human)

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REFERENCE
AUTHORS Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.,
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V.,
O'Hare,M.J., Soares,F., Brentani,R., Reis,D.F., de Souza,S.J. and
Simpson,A.J.
TITLE Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
MEDLINE 20202663
PUBMED 10737800
COMMENT Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=&t=IL3-CT0219-160
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High quality sequence stop: 660.
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SmaI; A mini-library was made by cloning products derived
from ORESTES PCR (U.S. Letters Patent application No.
196,716 - Ludwig Institute for Cancer Research) profiles
into the puc 18 vector. Reverse transcription of tissue
mRNA and cDNA amplification were performed under low
stringency conditions."

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FEATURES

source

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LOCUS IL3-CT0219-191199-030-E11 CT0219 Homo sapiens cDNA, mRNA sequence.
DEFINITION AW377012
ACCESSION AW377012
VERSION AW377012.1 GI:6881675
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 665)
HCGP http://www.ludwig.org.br/ORESTES.
The FAPESP/LICR Human Cancer Genome Project
Unpublished (1999)
Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=&t=IL3-CT0219-160
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SmaI; A mini-library was made by cloning products derived
from ORESTES PCR (U.S. Letters Patent application No.
196,716 - Ludwig Institute for Cancer Research) profiles
into the puc 18 vector. Reverse transcription of tissue
mRNA and cDNA amplification were performed under low
stringency conditions."

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ORIGIN

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Query Match 25.2%; Score 658.6; DB 10; Length 668;
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DEFINITION AW377012
ACCESSION AW377012
VERSION AW377012.1 GI:6881675
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 665)
HCGP http://www.ludwig.org.br/ORESTES.
The FAPESP/LICR Human Cancer Genome Project
Unpublished (1999)
Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=&t=IL3-CT0219-160
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SmaI; A mini-library was made by cloning products derived
from ORESTES PCR (U.S. Letters Patent application No.
196,716 - Ludwig Institute for Cancer Research) profiles
into the puc 18 vector. Reverse transcription of tissue
mRNA and cDNA amplification were performed under low
stringency conditions."

```

Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=IL3&t2=IL3-CT0219-191193-030-ELL&t3=1999-11-19&t4=1)
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FEATURES
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ORIGIN

Query Match 24.7%; Score 644.8; DB 10; Length 665;
Best Local Similarity 98.2%; Pred. No. 1.3e-88;
Matches 652; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

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DEFINITION AW604216
ACCESSION AW604216
VERSION AW604216.1 GI:7308957
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE
1 (bases 1 to 652)
HCGP http://www.ludwig.org.br/ORESTES.
AUTHORS The FAPESP/LICR Human Cancer Genome Project
TITLE Unpublished (1999)
JOURNAL
COMMENT Laboratory of Cancer Genetics
Contact: Simpson A.J.G.
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil

FEATURES
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ORIGIN

Query Match 24.3%; Score 633.2; DB 10; Length 652;
Best Local Similarity 98.9%; Pred. No. 7.4e-87;
Matches 646; Conservative 0; Mismatches 6; Indels 1; Gaps 1;

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QY 1396 TGGCTGTGCTGGTTGGAGCAGGAATGGGGTCACCCCTTTGCTTCTATCTTGAATCCA 1455
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RESULT 7

AW850616 618 bp mRNA linear EST 19-MAY-2000

LOCUS IL3-CT0219-160200-063-C10 CT0219 Homo sapiens cDNA, mRNA sequence.

DEFINITION AW850616

ACCESSION AW850616.1 GI:7946133

VERSION EST.

KEYWORDS Homo sapiens (human)

SOURCE Homo sapiens

ORGANISM Homo sapiens

REFERENCE Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

AUTHORS 1 (bases 1 to 618)

Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Simpson,A.J.

TITLE Shotgun sequencing of the human transcriptome with ORF expressed sequence tags

JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)

MEDLINE 20202663

PUBMED 10737800

COMMENT Contact: Simpson A.J.G.

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Tel: +55-11-2704922

Fax: +55-11-2707001

Email: asimpson@ludwig.org.br

This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (<http://www.ludwig.org.br/scripts/gethtml2.pl?tl=&t2=IL3-CT0219-160200-063-C10&t3=2000-02-16&t4=1>)

Seq primer: puc 18 forward

High quality sequence stop: 565.

Location/Qualifiers

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/dev_stage="Adult"

/clone_lib="CT0219"

/notes="Organ: colon; Vector: puc18; Site:1: SmaI; Site:2: SmaI; A mini-library was made by cloning products derived

FEATURES

source

from ORBESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

ORIGIN

Query Match 23.6%; Score 614.8; DB 10; Length 618;

Best Local Similarity 99.7%; Pred. No. 4.8e-84;

Matches 616; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1156 TCAGCATGGAAGTGGGCGAGTATATCTTTGTTAAATGCCCCCAATCTCTCTCGGAAT 1215

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QY 1216 GGATCTCTTTTACTTTTGACCTCTGCCAGAGAGATTTCTTCTCCATTCATATCCGAG 1275

Db 61 GGATCTCTTTTACTTTTGACCTCTGCCAGAGAGATTTCTTCTCCATTCATATCCGAG 120

QY 1276 CAGCAGGGGACTGGACAGAAATCTCATAGGGCTTTTCGAACCAACAATATTCACCAATTC 1335

Db 121 CAGCAGGGGACTGGACAGAAATCTCATAGGGCTTTTCGAACCAACAATATTCACCAATTC 180

QY 1336 CAGGATTTGAAGTGGATGGTCCCTTTGGGACAGCCAGTGGAGATGTTTCCAGTATGAAG 1395

Db 181 CAGGATTTGAAGTGGATGGTCCCTTTGGCAGCAGCCAGTGGATGTTGTCAGTATGAAG 240

QY 1396 TGGCTGTGCTGGTTGGAGCAGGAATTTGGGTGCACCCCTTTGCTTCTATCTTGAATCCA 1455

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Db 421 AGGAGATGGAGGAATTAGGCAAAAGTGGTTCCTTAAACTACCGTCTCTTCTCACCGGAT 480

QY 1636 GGACAGCAATATTGTTGGTTCAGCAGCATTAACCTTTGACAAAGGCCACTGACATCGTA 1695

Db 481 GGACAGCAATATTGTTGGTTCAGCAGCATTAACCTTTGACAAAGGCCACTGACATCGTA 540

QY 1696 CAGGTCTGAAACAGAAACCTCTTTGGGAGACCAATGTGGGACAAATGAGTTTCTACAA 1755

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RESULT 8

AW752752/c

LOCUS AW752752

DEFINITION IL3-CT0219-221199-029-G09 CT0219 Homo sapiens cDNA, mRNA sequence.

ACCESSION AW752752

VERSION AW752752.1 GI:7667684

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

AUTHORS 1 (bases 1 to 695)

Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and

Simpson A.J.
Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
MEDLINE 20202663
PUBMED 10737800
COMMENT Contact: Simpson A.J.G.
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Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=IL3&t2=IL3-CT0219-
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Seq primer: puc 18 forward
High quality sequence start: 21
High quality sequence stop: 618.

FEATURES

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/db_xref="taxon:9606"
/dev_stage="Adult"
/clone_lib="CT0219"
/note="Organ: colon; Vector: puc18; Site 1: SmaI; Site 2:
SmaI; A mini-library was made by cloning products derived
from ORESTES PCR (U.S. Letters Patent application No.
196,716 - Ludwig Institute for Cancer Research) profiles
into the pUC 18 vector. Reverse transcription of tissue
mRNA and cDNA amplification were performed under low
stringency conditions."

ORIGIN

Query Match 23.6%; Score 614.6; DB 10; Length 695;
Best Local Similarity 91.4%; Pred. No. 4.8e-84;
Matches 684; Conservative 0; Mismatches 7; Indels 57; Gaps 1;
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Db 695 ACCAACCCTCAAAACAAAAGATCTATTTCTACTGGATCTGACGGAGACAGGTGCT 636
Qy 1540 TTTCTGGTTCAACACTGTTGACTTCCCTGGACAGGACATGAGGAATTAGCAAG 1599
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Db 575 TGGGTTTCTAACTACCGTCTCTTCTCCACCGATGGACAGCAATATTGTTGTCATG 516
Qy 1660 CAGATTAACTTTGACAAGCCCACTGACATCGTGACAGGTCTGAAACAGAAAACCTCCT 1719
Db 515 CAGATTAACTTTGACAAGCCCACTGACATCGTGACAGGTCTGAAACAGAAAACCTCCT 456
Qy 1720 TTGGGAGACCAATGGGACAAATGAGTTTCTCAATAGCTACCTCCACCCCAAGTCTG 1779
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Qy 1780 TAGTGGGAGTTTCTTATGTGGCCCTCGACTTTGGCAAAGAGCTGGCAAATGCTGTC 1839
Db 395 TAGTGGGAGTTTCTTATGTGGCCCTCGACTTTGGCAAAGAGCTGGCAAATGCTGTC 336
Qy 1840 ACCGATATTCAGTCTGGATCCTAGAAAGGTTCAATTTACTTCAACAAAGAAAATTTT 1899
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Qy 1900 GAGTTATAGGAATAGGACGGTAATCTGCATTTTGTCTCTTTGTATCTTTCAGTAATTGAG 1959
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RESULT 9

AW604206 607 bp mRNA linear EST 23-MAR-2000
LOCUS IL3-CT0219-21C100-059-C11 CT0219 Homo sapiens cDNA, mRNA sequence.
ACCESSION AW604206
VERSION AW604206.1 GI:7308947
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 607)
AUTHORS HCGP http://www.ludwig.org.br/ORESTES.
TITLE The FAPESP/LICR Human Cancer Genome Project
JOURNAL Unpublished (1999)
COMMENT Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=IL3&t2=IL3-CT0219-
210100-059-C11&t3=2000-01-21&t4=1)
Seq primer: puc 18 forward
High quality sequence stop: 606.

FEATURES

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/db_xref="taxon:9606"
/dev_stage="Adult"
/clone_lib="CT0219"
/note="Organ: colon; Vector: puc18; Site 1: SmaI; Site 2:
SmaI; A mini-library was made by cloning products derived
from ORESTES PCR (U.S. Letters Patent application No.
196,716 - Ludwig Institute for Cancer Research) profiles
into the pUC 18 vector. Reverse transcription of tissue
mRNA and cDNA amplification were performed under low
stringency conditions."

ORIGIN

Query Match 23.2%; Score 605.4; DB 10; Length 607;
Best Local Similarity 99.8%; Pred. No. 1.3e-82;
Matches 606; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1156 TCACATGAGATGGGCGCATATATCTTTGTAATTCGCCCTCAATCTCTCTCTCGGAAT 1215
Db 1 TCACATGGAAGTGGGCGCATATATCTTTGTAATTCGCCCTCAATCTCTCTCTCGGAAT 60

QY 1216 GGATCTCTTTTACTTTTACCTCTGCTCCAGAGGAGATTTCTTCTCATTCATATCCGAG 1275
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 QY 1276 CAGCAGGGGACTGCACAGAGAAATCTCATAGGGGCTTTGCAACAACATATTCACCAATTC 1335
 Db 121 CAGCAGGGGACTGCACAGAGAAATCTCATAGGGGCTTTGCAACAACATATTCACCAATTC 180
 QY 1336 CCAGGATGAAGTGGATGGTCCCTTTGGCACAGCCAGTGAGGATGTTTCCAGTATGAAG 1395
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 QY 1396 TGGCTGTGCTGGTGGAGCAGGAATGGGTGTCACCCCTTTGCTTCTATCTTGAATCCA 1455
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 QY 1456 TCTGGTCAAAATTCAGTGTGCAGACCAACCACTCAAAAACAAAAGATCTATTCTACT 1515
 Db 301 TCTGGTCAAAATTCAGTGTGCAGACCAACCACTCAAAAACAAAAGATCTATTCTACT 360
 QY 1516 GGATCTGCAGGGAGACAGGTGGCTTTTCTGGTTTCAACAACCTGTGACTTCCCTGGAAC 1575
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 QY 1576 AGGAGATGGAGGAATAGGCAAGTGGTCTTCTAACTACCGTCTTCTCTCACCGAT 1635
 Db 421 AGGAGATGGAGGAATAGGCAAGTGGTCTTCTAACTACCGTCTTCTCTCACCGAT 480
 QY 1636 GGGACAGCAATATTTGTTGTCATGCAGCATTAACCTTTGCAAGGCCACTGCATCTGA 1695
 Db 481 GGGACAGCAATATTTGTTGTCATGCAGCATTAACCTTTGCAAGGCCACTGCATCTGA 540
 QY 1696 CAGGCTGAAACAGAAAACCTCTTTGGGAGACCAATGTGGGCAATGAGTTTTCTACAA 1755
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 Db 601 TAGCTAC 607

RESULT 10

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 LOCUS 618 bp mRNA linear EST 19-MAY-2000
 DEFINITION IL3-CT0219-160200-063-G06 CT0219 Homo sapiens cDNA, mRNA sequence.
 ACCESSION AW850625
 VERSION AW850625.1 GI:7946142
 KEYWORDS EST.
 SOURCE Homo sapiens (human)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 618)
 Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
 Nagai,M.A., da Silva W. Jr., Zago,M.A., Bordin,S., Costa,F.,
 Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
 Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V.,
 O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
 Simpson,A.J.
 Shotgun sequencing of the human transcriptome with ORF expressed
 sequence tags

TITLE

Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
 200202663
 10737800
 Contact: Simpson A.J.G.
 Laboratory of Cancer Genetics
 Ludwig Institute for Cancer Research

JOURNAL

MEDLINE
 PUBMED
 COMMENT
 Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
 Brazil
 Tel: +55-11-2704922
 Fax: +55-11-2707001
 Email: asimpson@ludwig.org.br

This sequence was derived from the FAPESP/LICR Human Cancer Genome
 Project. This entry can be seen in the following URL
 (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=et2-IL3-CT0219-160
 200-063-G06&t3=2000-02-16&t4=1)

Seq primer: puc 18 forward
 High quality sequence stop: 617.
 Location/Qualifiers

FEATURES

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 /dev_stage="Adult"
 /clone_lib="CT0219"
 /notes="Organ: colon; Vector: puc18; Site 1: SmaI; Site 2:
 SmaI; A mini-library was made by cloning products derived
 from ORESTES PCR (U.S. Letters Patent application No.
 196,716 - Ludwig Institute for Cancer Research) profiles
 into the puc 18 vector. Reverse transcription of tissue
 mRNA and cDNA amplification were performed under low
 stringency conditions."

ORIGIN

Query Match 23.1%; Score 601.8; DB 10; Length 618;
 Best Local Similarity 99.4%; Pred. No. 4.5e-82;
 Matches 614; Conservative 0; Mismatches 3; Indels 1; Gaps 1;
 QY 1156 TCAGCATGGAAGTGGGCGAGTATATCTTTGTTAAAT-GGCCCTCAATCTCTCTCCCTGGAA 1214
 Db 1 TCAGCATGGAAGTGGGCGAGTATATCTTTGTTAAATAGCCCTCAATCTCTCTCCCTGGAA 60
 QY 1215 TGGCATCTTTTACTTTTGACCTCTGCTCCAGAGGAAGATTTCTTCCATTCATATCCGA 1274
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 QY 1635 TGGGACAGCAATATTTGTTGTCATGCAGCATTAACCTTTGACAGGCCACTGCATCTG 1694
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 QY 1695 ACAGGTCTGAAACAGAAAACCTCTTTGGGAGACCAATGTGGGACCAATGAGTTTCTTACA 1754
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 QY 1755 ATAGTACTCTCCACCCC 1772
 Db 601 ATAGTACTCTCCACCCC 618

RESULT 11
 AW604209

LOCUS AW604209 605 bp mRNA linear EST 23-MAR-2000
DEFINITION IL3-CT0219-210100-059-E04 CT0219 Homo sapiens cDNA, mRNA sequence.
ACCESSION AW604209
VERSION AW604209.1 GI:7308950
SOURCE EST.
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
REFERENCE 1 (bases 1 to 605)
HCCP <http://www.ludwig.org.br/ORESTES>.
AUTHORS The FAPESP/LICR Human Cancer Genome Project
TITLE Unpublished (1999)
JOURNAL
COMMENT Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(<http://www.ludwig.org.br/scripts/gethtml2.pl?tl=IL3&t2=IL3-CT0219-210100-059-E04&t3=2000-01-21&t4=1>)
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High quality sequence stop: 552.
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/dev_stage="Adult"
/clone_lib="CT0219"
/note="Organ: colon; Vector: puc18; Site 1: SmaI; Site 2:
SmaI; A mini-library was made by cloning products derived
from ORESTES PCR (U.S. Letters Patent application No.
196,716 - Ludwig Institute for Cancer Research) profiles
into the pUC 18 vector. Reverse transcription of tissue
mRNA and cDNA amplification were performed under low
stringency conditions."

ORIGIN
Query Match 22.9%; Score 597.2; DB 10; Length 605;
Best Local Similarity 99.0%; Pred No. 2.3e-81;
Matches 599; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
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DB 1 TCAGCATGGAAGTGGGCGAGTATATCTTTGTTAATTCCTCAATCTCTCTCTGGAAT 60
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QY 1516 GGATCTGAGGAGACAGGTGCTTTTCTGGTTCACAACTGTGATTCCTCCCTGGAAC 1575
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DB 601 TAGCT 605
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AK053920 3242 bp mRNA linear HTC 20-SEP-2003
LOCUS AK053920
DEFINITION Mus musculus 2 days pregnant adult female oviduct cDNA, RIKEN
full-length enriched library, clone:E230001H16 product:cytochrome
b-245, beta polypeptide, full insert sequence.
ACCESSION AK053920
VERSION AK053920.1 GI:26343872
KEYWORDS HTC; CAP trapper.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1
Carninci P. and Hayashizaki Y.
High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
99279253
PUBMED 10349636
2
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Itoh M., Konno H., Okazaki Y., Muramatsu M. and Hayashizaki Y.
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prepare full-length cDNA libraries for rapid discovery of new genes
Genome Res. 10 (10), 1617-1630 (2000)
20499374
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3
Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
Konno H., Akiyama J., Nishi K., Kitsuai T., Tashiro H., Itoh M.,
Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
Okazaki Y., Muramatsu M., Inoue Y., Kira A. and Hayashizaki Y.
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sequencing pipeline with 384 multipillar sequencer
Genome Res. 10 (11), 1757-1771 (2000)
20530913
PUBMED 11076861
4
The RIKEN Genome Exploration Research Group Phase II Team and the
FANTOM Consortium.
Functional annotation of a full-length mouse cDNA collection
Nature 409, 685-690 (2001)
5
The FANTOM Consortium and the RIKEN Genome Exploration Research
Group Phase I & II Team.
Analysis of the mouse transcriptome based on functional annotation
of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)
6 (bases 1 to 3242)
Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,

Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Okazaki, Y., Saito, R., Satoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shingawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Takeda, Y., Tanaka, T., Tomaru, A., Toyota, T., Yasunishi, A., Yuramatsu, M. and Hayashizaki, Y.

Direct Submission

Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; Japan (1-72 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-res@gsc.riken.go.jp, URL: <http://genome.gsc.riken.go.jp/>, Tel: 81-45-503-9222, Fax: 81-45-503-9216)

cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.

Please visit our web site for further details.

URL: <http://genome.gsc.riken.go.jp/>

URL: <http://fantom.gsc.riken.go.jp/>

FEATURES
source

source

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 VERSION AW376980.1 GI:6881643
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 HCGP <http://www.ludwig.org.br/ORESTES>.
 TITLE The FAPESP/LICR Human Cancer Genome Project
 JOURNAL Unpublished (1999)
 COMMENT Contact: Simpson A.J.G.
 Laboratory of Cancer Genetics
 Ludwig Institute for Cancer Research
 Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
 Brazil
 Tel: +55-11-2704922
 Fax: +55-11-2707001
 Email: asimpson@ludwig.org.br
 This sequence was derived from the FAPESP/LICR Human Cancer Genome
 Project. This entry can be seen in the following URL
 (<http://www.ludwig.org.br/scripts/gethtml2.pl?cl=IL3&t2=IL3-CT0219-161199-031-G04&t3=1999-11-16&t4=1>)
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from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

ORIGIN

Query Match 22.3%; Score 580.6; DB 10; Length 588;
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 1 (bases 1 to 4000)
 Strausberg, R.
 Direct Submission
 TITLE Submitted (02-JAN-2003) National Institutes of Health, Mammalian
 JOURNAL Gene Collection (MGC), Cancer Genomics Office, National Cancer
 Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
 USA
 NIH-MGC Project URL: <http://mgc.nci.nih.gov>
 REMARK Contact: MGC help desk

Db 1658 GAAGCCTTGGCTAAACCTCTCAGTAAACAGAGCATCTCCAACCTCAGAACTCCGGCCGCGT 1717
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 REFERENCE 1 (bases 1 to 583)
 AUTHORS Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., deOliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.
 TITLE Shotgun sequencing of the human transcriptome with ORF expressed sequence tags
 JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
 MEDLINE 20202663
 PUBMED 10737800
 COMMENT Contact: Simpson A.J.G.
 Laboratory of Cancer Genetics
 Ludwig Institute for Cancer Research
 Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil
 Tel: +55-11-2704922
 Fax: +55-11-2707001
 Email: asimpson@ludwig.org.br
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FEATURES
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